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301 GTRKVTLHCETORDSLRTLYRFYHEGVPLRHKSVRCERGASISFSLTTTENSNGNYCTADNG 360
Db      |||
301 GTRKVTLHCETORDSLRTLYRFYHEGVPLRHKSVRCERGASISFSLTTTENSNGNYCTADNG 360
QY      |||
361 LGAKPSKAVSLSVTVPSHPVNLNLSPEGLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Db      |||
361 LGAKPSKAVSLSVTVPSHPVNLNLSPEGLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
QY      |||
421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPQRKAVSLITVPVSHPVLTLSA 480
Db      |||
421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPQRKAVSLITVPVSHPVLTLSA 480
QY      |||
481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSGRVVSFSLTEGHSNGY 540
Db      |||
481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSGRVVSFSLTEGHSNGY 540
QY      |||
541 CTADNGFGPQRSEVSLFVTVPSRPILTLRPRAQAVVGDLLLELHCEAPRGSPILYWF 600
Db      |||
541 CTADNGFGPQRSEVSLFVTVPSRPILTLRPRAQAVVGDLLLELHCEAPRGSPILYWF 600
QY      |||
601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPSRPI 660
Db      |||
601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPSRPI 660
QY      |||
661 LTRAPRAQAVVGDLLLELHCEALRGSSPILYRFYHEDVTLGKISAPSGGASFNLSLTT 720
Db      |||
661 LTRAPRAQAVVGDLLLELHCEALRGSSPILYRFYHEDVTLGKISAPSGGASFNLSLTT 720
QY      |||
721 HSGIYSCDADNGLEAQRSEMTLKVAVPVSRPVLTLRAPGTHAAVGDLLLELHCEALRG 780
Db      |||
721 HSGIYSCDADNGLEAQRSEMTLKVAVPVSRPVLTLRAPGTHAAVGDLLLELHCEALRG 780
QY      |||
781 LILYRFFHEDVTLGNRSSPGGASLNLSTAEHSGNYSCEADNGLGCAQRSETVTLITGL 840
Db      |||
781 LILYRFFHEDVTLGNRSSPGGASLNLSTAEHSGNYSCEADNGLGCAQRSETVTLITGL 840
QY      |||
841 TANRSGPFATGVAGGLTAGLAAGALLLYCMLSRKAGKPKASDPARSPSDSDSEPIYH 900
Db      |||
841 TANRSGPFATGVAGGLTAGLAAGALLLYCMLSRKAGKPKASDPARSPSDSDSEPIYH 900
QY      |||
901 NVPAWELQPVYTNANPRGENVYSEVRIIOEKKHVAASDPRLRNKGPSPIIYSEVKVA 960
Db      |||
901 NVPAWELQPVYTNANPRGENVYSEVRIIOEKKHVAASDPRLRNKGPSPIIYSEVKVA 960
QY      |||
961 STPVSGSLFLASSAPHR 977
Db      |||
961 STPVSGSLFLASSAPHR 977

RESULT 2
Q8NF56 PRELIMINARY; PRT; 437 AA.
AC Q8NF56;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE FLJ00333 protein (Fragment).
GN Name=FLJ00333;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Jikuya H., Iakano J., Kikuno R., Nagase T., Ohara O.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK090423; BAC03404.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 3.

DR PROSITE; PS50835; IG-LIKE; 3.
FT NON TER 1
SQ SEQUENCE 437 AA; 46521 MW; F56DED36523E52CA CRC64;

Query Match 41.2%; Score 403; DB 2; Length 437;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 575 AQAVVGDLLLELHCEAPRGSPILYWFYHEDVTLGSSAPSGGEASFNLSLTAHSGNYS 634
Db 575 AQAVVGDLLLELHCEAPRGSPILYWFYHEDVTLGSSAPSGGEASFNLSLTAHSGNYS 634
QY 635 EANNGLVAQHSDDTISLSVIVPSRPILTLRAPGTHAAVGDLLLELHCEALRGSPILYWF 694
Db 635 EANNGLVAQHSDDTISLSVIVPSRPILTLRAPGTHAAVGDLLLELHCEALRGSPILYWF 694
QY 95 EANNGLVAQHSDDTISLSVIVPSRPILTLRAPGTHAAVGDLLLELHCEALRGSPILYWF 154
Db 95 EANNGLVAQHSDDTISLSVIVPSRPILTLRAPGTHAAVGDLLLELHCEALRGSPILYWF 154
QY 695 HEDVTLGKISAPSGGASFNLSLTTTETSHSGIYSCDADNGLEAQRSEMTLKVAVPVSRPV 754
Db 695 HEDVTLGKISAPSGGASFNLSLTTTETSHSGIYSCDADNGLEAQRSEMTLKVAVPVSRPV 754
QY 755 TLRAPGTHAAVGDLLLELHCEALRGSPILYRFYHEDVTLGKISAPSGGASFNLSLTAH 814
Db 755 TLRAPGTHAAVGDLLLELHCEALRGSPILYRFYHEDVTLGKISAPSGGASFNLSLTAH 814
QY 215 TLRAPGTHAAVGDLLLELHCEALRGSPILYRFYHEDVTLGKISAPSGGASFNLSLTAH 274
Db 215 TLRAPGTHAAVGDLLLELHCEALRGSPILYRFYHEDVTLGKISAPSGGASFNLSLTAH 274
QY 815 GNYSCDADNGLGCAQRSETVTLITGLTANRSGPFATGVAGGLSIAGLAAGALLLYCMLS 874
Db 815 GNYSCDADNGLGCAQRSETVTLITGLTANRSGPFATGVAGGLSIAGLAAGALLLYCMLS 874
QY 875 RKAGRKPAASPPASPSDSQSEPTNYNVPAWELQPVYTNANPRGENVYSEVRIIOEKK 934
Db 875 RKAGRKPAASPPASPSDSQSEPTNYNVPAWELQPVYTNANPRGENVYSEVRIIOEKK 934
QY 935 KHAVASDPRLRNKGPSPIIYSEVKVASTPVSGSLFLASSAPHR 977
Db 935 KHAVASDPRLRNKGPSPIIYSEVKVASTPVSGSLFLASSAPHR 977

RESULT 3
Q6UY46 PRELIMINARY; PRT; 124 AA.
AC Q6UY46;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IRTA2.
GN ORENAMES=UNQ503;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.F., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie B., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358085; AA088452.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
SQ SEQUENCE 124 AA; 14080 MW; D7915849A385455D CRC64;
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Query Match 10.4%; Score 102; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.4e-90;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWILLVLAPVSGQFARTPRPIIFLOPPPTWTFQGERVLTCKGFRFYSPQTKWYHR 60
DB 1 MLLWILLVLAPVSGQFARTPRPIIFLOPPPTWTFQGERVLTCKGFRFYSPQTKWYHR 60

QY 61 YLGKEILRETPDNILEVQESGYRCQAQGSPLSSPVHLDFSS 102
DB 61 YLGKEILRETPDNILEVQESGYRCQAQGSPLSSPVHLDFSS 102

RESULT 4
ID AAQ88452 PRELIMINARY; PRT; 124 AA.
AC AAQ88452;
DT 02-WAR-2004 (TREMBLrel. 27, Created)
DT 02-WAR-2004 (TREMBLrel. 27, Last sequence update)
DT 02-WAR-2004 (TREMBLrel. 27, Last annotation update)
DE IRTA2.
GN UNQ503.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klinowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
RT Bioinformatics Assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358085; AAQ88452.1; -.
SQ SEQUENCE 124 AA; 14080 MW; D7915849A385455D CRC64;

Query Match 10.4%; Score 102; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.4e-90;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWILLVLAPVSGQFARTPRPIIFLOPPPTWTFQGERVLTCKGFRFYSPQTKWYHR 60
DB 1 MLLWILLVLAPVSGQFARTPRPIIFLOPPPTWTFQGERVLTCKGFRFYSPQTKWYHR 60

QY 61 YLGKEILRETPDNILEVQESGYRCQAQGSPLSSPVHLDFSS 102
DB 61 YLGKEILRETPDNILEVQESGYRCQAQGSPLSSPVHLDFSS 102

RESULT 5
ID Q9BZ14 PRELIMINARY; PRT; 144 AA.
AC Q9BZ14;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE SH2 domain-containing phosphatase anchor protein 1c.
GN Name=SPAP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
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Query Match 2.4%; Score 23; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.9e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 ASFNLSLTAEHSGNYSCAANNGL 640
DB 99 ASFNLSLTAEHSGNYSCAANNGL 121

RESULT 6
ID Q9BZ15 PRELIMINARY; PRT; 192 AA.
AC Q9BZ15;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE SH2 domain-containing phosphatase anchor protein 1b.
GN Name=SPAP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092675; PubMed=11162587;
RA Xu M., Zhao R., Zhao Z.J.;
RT "Molecular Cloning and Characterization of SPAP1, an Inhibitory
RT Receptor.";
RL Biochem. Biophys. Res. Commun. 280:768-775(2001).
DR GO; AF319439; AAK01403.1; -.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0007267; P:cell-cell signaling; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG_1.
DR PROSITE; PSS0835; IG_LIKE; 1.
SQ SEQUENCE 192 AA; 20680 MW; C9962BBB4B15B08D CRC64;

Query Match 2.4%; Score 23; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 2.5e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 ASFNLSLTAEHSGNYSCAANNGL 640
DB 99 ASFNLSLTAEHSGNYSCAANNGL 121

RESULT 7
ID Q9BZ16 PRELIMINARY; PRT; 255 AA.
AC Q9BZ16;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE SH2 domain-containing phosphatase anchor protein 1a (IFGP4).
GN Name=SPAP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092675; PubMed=11162587;
RA Xu M., Zhao R., Zhao Z.J.;
RT "Molecular Cloning and Characterization of SPAP1, an Inhibitory
RL Receptor.";
RL Biochem. Biophys. Res. Commun. 280:768-775(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Tonsil;
RX MEDLINE=22033006; PubMed=12037601;
RA Guseinikov S.V., Ershova S.A., Mechetina L.V., Najakshin A.M.,
RA Volkova O.Y., Alabyev B.I., Taranin A.V.;
RT "A family of highly diverse human and mouse genes structurally links
RL leukocyte FcR, gp42 and PECAM-1.";
RT Immunogenetics 54:87-95(2002).
DR EMBL; AF319438; AAK01402.1; -.
DR EMBL; AF390037; AAM12152.1; -.
DR PIR; JC7593; JC7593.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0005070; F:SH3/SH2 adaptor protein activity; IPI.
DR GO; GO:0007267; P:cell-cell signaling; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 255 AA; 27546 MW; 82556447FB6BAB14 CRC64;

Query Match 2.4%; Score 23; DB 2; Length 255;
Best Local Similarity 100.0%; Pred. No. 3.2e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 618 ASFNLSLTAEHSGNSYSCEANNGL 640
Db 99 ASFNLSLTAEHSGNSYSCEANNGL 121

RESULT 8
Q96LA5 PRELIMINARY; PRT; 508 AA.
ID Q96LA5
AC Q96LA5 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Fc receptor-like protein 2 (FCRH2).
GN Name=FCRH2; ORFNames=UNQ9236;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396562; PubMed=11493702;
RA Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;
RT "Identification of a family of Fc receptor homologs with preferential
RL B cell expression.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396562; PubMed=11493702;
RA Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;
RT "Identification of a family of Fc receptor homologs with preferential
RL B cell expression.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).

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DR EMBL; AY043465; AAK91778.1; -.
DR EMBL; AY358130; AAK88497.1; -.
DR HSP; P12319; IF2Q.
DR Genew; HGNC:14875; SPAP1.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 3.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Receptor.
SQ SEQUENCE 508 AA; 55541 MW; 9AB30E0411B41EDC CRC64;

Query Match 2.4%; Score 23; DB 2; Length 508;
Best Local Similarity 100.0%; Pred. No. 5.8e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 618 ASFNLSLTAEHSGNSYSCEANNGL 640
Db 352 ASFNLSLTAEHSGNSYSCEANNGL 374

RESULT 9
AAQ88497 PRELIMINARY; PRT; 508 AA.
ID AAQ88497
AC AAQ88497 (TEMBLrel. 27, Created)
DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
DE FCRH2.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
RT Bioinformatics Assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358130; AAK88497.1; -.
SQ SEQUENCE 508 AA; 55541 MW; 9AB30E0411B41EDC CRC64;

Query Match 2.4%; Score 23; DB 2; Length 508;
Best Local Similarity 100.0%; Pred. No. 5.8e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 618 ASFNLSLTAEHSGNSYSCEANNGL 640
Db 352 ASFNLSLTAEHSGNSYSCEANNGL 374

RESULT 10
Q96P30 PRELIMINARY; PRT; 639 AA.
ID Q96P30
AC Q96P30 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE SH2 domain-containing phosphatase anchor protein 2b.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

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RN  SEQUENCE FROM N.A.
RP  Xu M.-J., Zhao R., Zhao Z.J.;
RA  Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RL  EMBL; AF416902; AAL13291.1; -.
DR  HSSP; P12319; 1F2Q.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003598; Ig c2.
DR  InterPro; IPR002052; N6_Mtase.
DR  Pfam; PF00047; Ig; 3.
DR  SMART; SM00408; IGC2; 1.
DR  PROSITE; PS50835; IG_LIKE; 5.
DR  PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
SQ  SEQUENCE 639 AA; 69928 MW; DEAD7AD4B64CA984 CRC64;

Query Match 1.7%; Score 17; DB 2; Length 639;
Best Local Similarity 100.0%; Pred. No. 5.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 ASFNLSLTAHSGNYSC 634
Db 340 ASFNLSLTAHSGNYSC 356
|||||

RESULT 11
ID Q96LA4 PRELIMINARY; PRT; 734 AA.
AC Q96LA4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fc receptor-like protein 3.
GN Name=FCRH3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396562; PubMed=11493702;
RA Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;
RT "Identification of a family of Fc receptor homologs with preferential
RT B cell expression.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777 (2001).
DR EMBL; AY043466; AAK9179.1; -.
DR HSSP; P12319; 1F2Q.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig c2.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 6.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 734 AA; 80827 MW; B359B494EBF12138 CRC64;

Query Match 1.7%; Score 17; DB 2; Length 734;
Best Local Similarity 100.0%; Pred. No. 5.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 ASFNLSLTAHSGNYSC 634
Db 435 ASFNLSLTAHSGNYSC 451
|||||

RESULT 12
ID Q96P31 PRELIMINARY; PRT; 734 AA.
AC Q96P31;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE FCRH3 protein.

```

```

DE SH2 domain-containing phosphatase anchor protein 2a.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu M.-J., Zhao R., Zhao Z.J.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF416901; AAL13290.1; -.
DR HSSP; P12319; 1F2Q.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig c2.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 6.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
SQ SEQUENCE 734 AA; 80855 MW; B3411B73A35EC668 CRC64;

Query Match 1.7%; Score 17; DB 2; Length 734;
Best Local Similarity 100.0%; Pred. No. 5.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 ASFNLSLTAHSGNYSC 634
Db 435 ASFNLSLTAHSGNYSC 451
|||||

RESULT 13
ID Q96P29 PRELIMINARY; PRT; 740 AA.
AC Q96P29;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SH2 domain-containing phosphatase anchor protein 2c.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu M.-J., Zhao R., Zhao Z.J.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF416903; AAL13292.1; -.
DR HSSP; P12319; 1F2Q.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig c2.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 6.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
SQ SEQUENCE 740 AA; 81440 MW; 038AFA83A2909E46 CRC64;

Query Match 1.7%; Score 17; DB 2; Length 740;
Best Local Similarity 100.0%; Pred. No. 5.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 ASFNLSLTAHSGNYSC 634
Db 441 ASFNLSLTAHSGNYSC 457
|||||

RESULT 14
ID Q8N6S2 PRELIMINARY; PRT; 742 AA.
AC Q8N6S2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE FCRH3 protein.

```

OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Collins B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussdin T.B., Teshnyuk S., Carrinai P., Prange C.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek A.M., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Murney D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywicki M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC028933; AAH28933.1; -
 DR HSSP; P12319; 1F20.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR002052; N6_Mtase.
 DR Pfam; PF00047; IG; 4.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS00835; IG LIKE; 6.
 DR PROSITE; PS00092; N6_MTASE; UNKNOWN 1.
 SQ SEQUENCE 742 AA, 31853 MW, B0650200E7CA19B8 CRC64;
 Query Match 1.7%; Score 17; DB 2; Length 742;
 Best Local Similarity 100.0%; Pred. No. 5.8e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 618 ASFNLSLTAHSGNSYC 634
 DB 435 ASFNLSLTAHSGNSYC 451
 RESULT 15
 Q8N759 PRELIMINARY; PRT; 366 AA.
 ID Q8N759
 AC Q8N759
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein FLJ39371.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=14702039;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,

RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Musashino K., Iwaki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiya H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Omori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togaashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuko Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 DR EMBL; AK096590; BAC04842.1; -
 DR GO; GO:0004872; Fireceptor activity; IEA.
 DR InterPro; IPR003599; IG-like.
 DR InterPro; IPR007110; IG-like.
 DR Pfam; PF00047; IG; 3.
 DR SMART; SM00409; IG; 3.
 DR PROSITE; PS00835; IG LIKE; 3.
 KW Receptor.
 SQ SEQUENCE 366 AA, 40434 MW, 6F79D0F9EBDE2AE0 CRC64;
 Query Match 1.5%; Score 15; DB 2; Length 366;
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 704 SAPSGGGASFNLSLT 718
 DB 253 SAPSGGGASFNLSLT 267

Search completed: November 18, 2004, 13:05:01
 Job time : 212 secs

FT /note= "putative consensus Src-homology 2 (SH2) binding
 FT domain"
 XX
 PN WO200138490-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 28-NOV-2000; 2000WO-US032403.
 XX
 PR 29-NOV-1999; 95US-0168151P.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Daila-Favera R;
 XX
 DR WPI; 2001-355921/37.
 XX
 DR N-PSDB; AAF30952.
 XX
 XX New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor
 PT Translocation Associated proteins, used to treat B cell malignancies
 PT including lymphomas and multiple myeloma.
 XX
 PS Claim 3; Fig 18B-1-18B-2; 72pp; English.
 XX
 CC The present sequence is that of the novel human immunoglobulin receptor,
 CC immunoglobulin superfamily receptor translocation associated protein
 CC isoform 2c (IRTA2c), an FC receptor involved in the pathogenesis of
 CC lymphoma and melanoma. Efforts to identify genes involved in chromosomal
 CC aberrations affecting band 1q21 in multiple myeloma and B cell lymphoma
 CC led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding
 CC members of a novel subfamily of related receptors within the
 CC immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA
 CC isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82313 and AAB82314).
 CC IRTA2c is the longest isoform. It is a type I transmembrane glycoprotein.
 CC Each SH2 binding site agrees with the immune receptor tyrosine-based
 CC inhibition motif (ITIM) consensus and is encoded by a separate exon. The
 CC IRTA genes display a specific pattern of expression in mature B cells,
 CC IRTA2 is expressed in GC centrocytes and in perifollicular cells, which
 CC may include immunoblasts and memory cells. The invention provides IRTA
 CC nucleic acids and proteins, and antibodies directed to epitopes of IRTA
 CC proteins. Methods are claimed for: detecting a B cell malignancy
 CC comprising a 1q21 chromosomal rearrangement using a nucleic acid molecule
 CC that specifically hybridises with a unique sequence of human IRTA1-5; and
 CC treating a subject having a B cell cancer by administering an anti-IRTA
 CC antibody or an antisense oligonucleotide that specifically hybridises to
 CC IRTA mRNA so as to prevent overexpression of IRTA protein and hence to
 CC arrest cell growth or induce cell death of cancer cells expressing IRTA.
 CC The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma,
 CC multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse
 CC large cell lymphoma and follicular lymphoma. The B cell lymphoma is
 CC selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-
 CC Hodgkin's lymphoma
 XX
 SQ Sequence 977 AA;

Query Match
 Best Local Similarity 100.0%; Score 977; DB 4; Length 977;
 Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPMTTVFQGERVTLTCKGRFYSPOKTKVHR 60
 DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPMTTVFQGERVTLTCKGRFYSPOKTKVHR 60

QY 61 YLGEKILRETPDNIIEVQSGEYRCQAQGSPLSPVHLDFSSALLIQLAPLSVEGDSV 120
 DB 61 YLGEKILRETPDNIIEVQSGEYRCQAQGSPLSPVHLDFSSALLIQLAPLSVEGDSV 120

QY 121 LECRAKAEVTLNNTYKQDNVLAFLNKRTDPhiPHACLKNGAYRCTGYKESCCPVSSNT 180
 DB 121 LECRAKAEVTLNNTYKQDNVLAFLNKRTDPhiPHACLKNGAYRCTGYKESCCPVSSNT 180

QY 181 VKIQVQEPFTRFVLRASSFQPIISGNPVTLTCTETQLSLERSDVPLRFRFRDDQTLGLGWS 240

DB 181 VKIQVQEPFTRFVLRASSFQPIISGNPVTLTCTETQLSLERSDVPLRFRFRDDQTLGLGWS 240
 QY 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIQVOIPASHPVLTLSPEKALNFE 300
 DB 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIQVOIPASHPVLTLSPEKALNFE 300
 QY 301 GTKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVCRCGASISFSLTSTNSGNYICTADNG 360
 DB 301 GTKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVCRCGASISFSLTSTNSGNYICTADNG 360
 QY 361 LGAKPSKAVLSLTVPVSHPVNLNLSPPEDLLFECAKVTLHCEAQRGSPIILYQFHEDAA 420
 DB 361 LGAKPSKAVLSLTVPVSHPVNLNLSPPEDLLFECAKVTLHCEAQRGSPIILYQFHEDAA 420
 QY 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
 DB 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
 QY 481 EALTPEGATVTLHCEVQRGSPOILYQFVHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
 DB 481 EALTPEGATVTLHCEVQRGSPOILYQFVHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
 QY 541 CTADNGFGPQRSEVVSFLFVTVPSRPILTLRVPRQAQVVGDLLELHCEAPRGSPPILYWF 600
 DB 541 CTADNGFGPQRSEVVSFLFVTVPSRPILTLRVPRQAQVVGDLLELHCEAPRGSPPILYWF 600
 QY 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTSLSVIVPSRPI 660
 DB 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTSLSVIVPSRPI 660
 QY 661 LTRAPRAQAVVGDLLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGGSFNLSTTE 720
 DB 661 LTRAPRAQAVVGDLLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGGSFNLSTTE 720
 QY 721 HSGIYSCDADNGLEAQRSEMVTLVAVPSRPVLTIRAPGTHAAVGDLELHCEALRGSP 780
 DB 721 HSGIYSCDADNGLEAQRSEMVTLVAVPSRPVLTIRAPGTHAAVGDLELHCEALRGSP 780
 QY 781 LLYLRFHEDVTLGNRSSPSGGASLNLSTLTAHSGNYSCEADNGLGAQRSETVLYITGL 840
 DB 781 LLYLRFHEDVTLGNRSSPSGGASLNLSTLTAHSGNYSCEADNGLGAQRSETVLYITGL 840
 QY 841 TANRSGPFATGVAGGLSTAGLAAGALLYLWCMSKAGRKSPADPARSPSDSDSQEPTYH 900
 DB 841 TANRSGPFATGVAGGLSTAGLAAGALLYLWCMSKAGRKSPADPARSPSDSDSQEPTYH 900
 QY 901 NVPAMEELQPVVTNANPRGENVYSEVRIIOBKKHAVASDPRLRNKGSPIIYSEVKVA 960
 DB 901 NVPAMEELQPVVTNANPRGENVYSEVRIIOBKKHAVASDPRLRNKGSPIIYSEVKVA 960
 QY 961 STPVSGSLFLASSAPHR 977
 DB 961 STPVSGSLFLASSAPHR 977

RESULT 2
 ADM35237
 ID ADM35237 standard; protein; 977 AA.
 XX
 AC ADM35237;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human LY1448P cancer related protein for cancer detection method.
 XX
 KW cytostatic; T-cell vaccine; detection; cancer;
 KW chronic lymphocytic leukemia.
 XX
 OS Homo sapiens.
 XX
 XX WO2003077836-A2.
 XX
 PD 25-SEP-2003.

XX PF 06-NOV-2002; 2002WO-US035728.
XX PR 06-NOV-2001; 2001US-00040862.
XX PR 23-MAY-2002; 2002US-00154884.
XX PA (CORI-) CORIXA CORP.
XX PI Gaiger A, Algate PA, Mannion J, Retter M;
XX DR WPI; 2003-756941/71.
XX
XX Detecting cancer in a patient comprises contacting a biological sample
XX PT from the patient with a binding agent that binds to a cancer-associated
XX PT polypeptide and comparing the amount of polypeptide to a predetermined
XX PT cutoff value.
XX PS Disclosure; SEQ ID NO 10462; 419pp; English.
XX
XX The invention relates to a method of detecting (M1) cancer in a patient
XX CC by: (i) contacting a biological sample from the patient with an agent
XX CC that binds to any of three polypeptides given in the specification; (ii)
XX CC detecting in a sample an amount of the peptide that binds to the binding
XX CC agent; and (iii) comparing the amount of polypeptide present in the
XX CC patient's sample to a predetermined cutoff value. The specification also
XX CC discloses a separate method for detecting (M2) cancer in a patient by a
XX CC method similar to M1, except that the detection agent is an
XX CC oligonucleotide that binds to any of three polynucleotides given in the
XX CC specification. M1 and M2 are useful for detecting the presence of cancer
XX CC in a patient, especially chronic lymphocytic leukemia. The applicants
XX CC have identified specific human polypeptides overexpressed in one or more
XX CC types of hematological malignancies. This sequence corresponds to a
XX CC protein used in the method of the invention.
XX
XX SQ Sequence 977 AA;

Query Match 100.0%; Score 977; DB 7; Length 977;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLWVILLVAPVSGQFARTPRPIIFLQPPWTVFQGERVTLCKGFRFYSPQTKWYHR 60
Db 1 MLLWVILLVAPVSGQFARTPRPIIFLQPPWTVFQGERVTLCKGFRFYSPQTKWYHR 60

Qy 61 YLGEILLREPDNLTLEQVSEGEVCECOAGGSLSPVHLDFSSASLILOAPLSVPEGDSVV 120
Db 61 YLGEILLREPDNLTLEQVSEGEVCECOAGGSLSPVHLDFSSASLILOAPLSVPEGDSVV 120

Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDPhiPHACLKONGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDPhiPHACLKONGAYRCTGYKESCCPVSSNT 180

Qy 181 VKIQVQEPFTRPVLRASSFPISGNFVTLTCTQLSLERSDVPURFRFRDDQTLGLWS 240
Db 181 VKIQVQEPFTRPVLRASSFPISGNFVTLTCTQLSLERSDVPURFRFRDDQTLGLWS 240

Qy 241 LSPNFQITAMWSKDSGFYCKAAATPHSVISDSRPSWIOQVIPASHPVLTLSPEKALNFE 300
Db 241 LSPNFQITAMWSKDSGFYCKAAATPHSVISDSRPSWIOQVIPASHPVLTLSPEKALNFE 300

Qy 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVRCERGASISFSLTTENSGNYCYTADNG 360
Db 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVRCERGASISFSLTTENSGNYCYTADNG 360

Qy 361 LGAKPSKAVSLSVTPVSHVPLNLSPPEDLIFEGAKVTLHCEAORGSLPILYOPHHEDAA 420
Db 361 LGAKPSKAVSLSVTPVSHVPLNLSPPEDLIFEGAKVTLHCEAORGSLPILYOPHHEDAA 420

Qy 421 LERRANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSA 480
Db 421 LERRANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSA 480

Qy 481 BALTFEGATVTLHCEVQSGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTECHSGNYY 540

Db 481 EALTPEGATVTLHCEVQSGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTECHSGNYY 540
Qy 541 CTADNGFGPQRSSEVVSFLVTVVPSRPILTLRVPRAQAVVGDILLEHCEAPRGSPILYWF 600
Db 541 CTADNGFGPQRSSEVVSFLVTVVPSRPILTLRVPRAQAVVGDILLEHCEAPRGSPILYWF 600
Qy 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPSRPI 660
Db 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPSRPI 660
Qy 661 LTFRAPRAQAVVGDILLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT 720
Db 661 LTFRAPRAQAVVGDILLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT 720
Qy 721 HSGIYSCADNGLEAQRSEMVTLKVAVPVSRPVLTLRAPGTHAAVGDILLEHCEALRGSP 780
Db 721 HSGIYSCADNGLEAQRSEMVTLKVAVPVSRPVLTLRAPGTHAAVGDILLEHCEALRGSP 780
Qy 781 LILYRPFHEDVTLGNRSSPSSGASLNLSLTAHSGNYSCEADNGLGAORSETVTLIITGL 840
Db 781 LILYRPFHEDVTLGNRSSPSSGASLNLSLTAHSGNYSCEADNGLGAORSETVTLIITGL 840
Qy 841 TANRSGPATGVAGGLLSIAGLAAGALLLYCWLRSKAGRKPDASDPARSPSDSDSOEPTYH 900
Db 841 TANRSGPATGVAGGLLSIAGLAAGALLLYCWLRSKAGRKPDASDPARSPSDSDSOEPTYH 900
Qy 901 NYPAMEELQPVYTNANPRGENVYSEVRIOBKXKHAVASDPRLHNRKSGSPIIYSEVKVA 960
Db 901 NYPAMEELQPVYTNANPRGENVYSEVRIOBKXKHAVASDPRLHNRKSGSPIIYSEVKVA 960
Qy 961 STPVSGSLFLASSAPHR 977
Db 961 STPVSGSLFLASSAPHR 977

RESULT 3
ABP97215
ID ABP97215 standard; protein; 977 AA.
XX
AC ABP97215;
XX
DT 01-JUL-2003 (first entry)
XX
DE Tumour-associated antigenic target protein TAT374 SEQ ID NO:97.
XX
KW Human; tumour-associated antigenic target; TAT; tumour; diagnosis;
XX cancer.
XX Homo sapiens.
XX
PN WO2003024392-A2.
XX
PD 27-MAR-2003.
XX
PF 11-SEP-2002; 2002WO-US028859.
XX
PR 18-SEP-2001; 2001US-0323268P.
PR 19-OCT-2001; 2001US-0339227P.
PR 07-NOV-2001; 2001US-0336827P.
PR 20-NOV-2001; 2001US-0331906P.
PR 02-JAN-2002; 2002US-0345444P.
PR 03-APR-2002; 2002US-0369724P.
PR 19-AUG-2002; 2002US-0404809P.
XX
PA (GETH) GENENTECH INC.
XX
PI Frantz G, Hillan KJ, Phillips HS, Polakis P, Spencer SD;
PI Williams PM, Wu TD, Zhang Z;
XX
XX WPI; 2003-354551/33.
DR N-PSDB; ACC49533.
XX

PT New antibodies against tumor-associated antigenic target polypeptide,
PT useful for treating or diagnosing tumors or cancers in mammals, e.g.
PT prostate cancer, lung cancer, prostate adenocarcinomas or renal cell
PT carcinomas.
XX
XX Claim 2; Fig 97; 285pp; English.
XX
CC ACC49493 to ACC49552 encode the human tumour-associated antigenic target
CC (TAT) proteins given in ABP97175 to ABP97234. The present invention
CC describes an isolated antibody that binds to a polypeptide having at
CC least 80 % sequence identity to any of the 60 150-800 residue amino acid
CC sequences (S1), given in ABP97175 to ABP97234, comprising (S1), lacking
CC its associated signal peptide, encoded by any of the 60 2000-3000 base
CC pair sequences (S2), given in ACC49493 to ACC49552. TAT proteins have
CC cytostatic activity. The antibody can be used for treating or diagnosing
CC tumours or cancers in mammals, e.g. prostate cancer, lung cancer, breast
CC cancer, colon cancer, ovarian cancer, prostate adenocarcinomas, renal
CC cell carcinomas, or thyroid cancer
XX
XX Sequence 977 AA;
SQ

Query Match 80.7%; Score 788; DB 6; Length 977;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 888; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVLTICKGRFFYSPOKTKVHR 60
Db 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVLTICKGRFFYSPOKTKVHR 60

QY 61 YLGKILRETPNILEVQESGEYRCQAQCSPLSPVHLDFSSASLILOAPLSVFEQSVV 120
Db 61 YLGKILRETPNILEVQESGEYRCQAQCSPLSPVHLDFSSASLILOAPLSVFEQSVV 120

QY 121 LRCRAKAEVTLNNTYKNDNLVAFLNKRTDPhiPACLNKGAVRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTYKNDNLVAFLNKRTDPhiPACLNKGAVRCTGYKESCCPVSSNT 180

QY 181 VKIQVQEPFTRPVLRASSFQPIGNSPVLTCTETQLSLERSDVPLRFRFRDDQTLGLWS 240
Db 181 VKIQVQEPFTRPVLRASSFQPIGNSPVLTCTETQLSLERSDVPLRFRFRDDQTLGLWS 240

QY 241 LSPNFQITAMWSKDSGFYWCACKAATPHSVISDSRSTQVQIPASHPVLTLSPEKALNFE 300
Db 241 LSPNFQITAMWSKDSGFYWCACKAATPHSVISDSRSTQVQIPASHPVLTLSPEKALNFE 300

QY 301 GPKVTLHCETQDSLRITLYRFYHEGVPLRHKSVCERGASISFSLTTENSGNYICTADNG 360
Db 301 GPKVTLHCETQDSLRITLYRFYHEGVPLRHKSVCERGASISFSLTTENSGNYICTADNG 360

QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPDLIFEGAKVTLHCEAQRGSLPILYQHHEHDA 420
Db 361 LGAKPSKAVSLSVTPVSHPVNLSSPDLIFEGAKVTLHCEAQRGSLPILYQHHEHDA 420

QY 421 LERRSANSAGGVAISFSLTAHSGNYICTADNGFQPSKAVSLITVPVSHPVLTLSA 480
Db 421 LERRSANSAGGVAISFSLTAHSGNYICTADNGFQPSKAVSLITVPVSHPVLTLSA 480

QY 481 EALTPEGATVTLHCEVQRGSQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
Db 481 EALTPEGATVTLHCEVQRGSQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540

QY 541 CTADNGFQPSRSEVSVLFTVPVSRPILTLVPRAQAVVGDLLHCEAPRGSPILYWF 600
Db 541 CTADNGFQPSRSEVSVLFTVPVSRPILTLVPRAQAVVGDLLHCEAPRGSPILYWF 600

QY 601 YHEDVTLGSSSAPSGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLIVPVSERPI 660
Db 601 YHEDVTLGSSSAPSGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLIVPVSERPI 660

QY 661 LTFRAPRAQAVVGDLLHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT 720
Db 661 LTFRAPRAQAVVGDLLHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT 720

QY 721 HSGIYSCADNGLGAQRSEWTLKVAVPVSRPVLTLRAPGTHAAVGDLLHCEALRGSP 780
Db 721 HSGIYSCADNGLGAQRSEWTLKVAVPVSRPVLTLRAPGTHAAVGDLLHCEALRGSP 780

QY 781 LILYRFFHEDVTLGNRSSPGGASLNLSLTAEHSGNYSCEADNGLGAQRSEWTLVITGL 840
Db 781 LILYRFFHEDVTLGNRSSPGGASLNLSLTAEHSGNYSCEADNGLGAQRSEWTLVITGL 840

QY 841 TANRSQPFATGVAGGLSLTAGLAAGALLYCWLRSKAGKPKASDPARSP 889
Db 841 TANRSQPFATGVAGGLSLTAGLAAGALLYCWLRSKAGKPKASDPARSP 889

RESULT 4
AAB82313
ID AAB82313 standard; protein; 759 AA.
XX
XX AAB82313;
XX
XX 23-JUL-2001 (first entry)
XX
XX Human immunoglobulin receptor isoform IRTA2a.
DE
XX Immunoglobulin superfamily receptor translocation associated; IRTA;
KW IRTA2a; human; immunoglobulin receptor; Fc receptor; melanoma; lymphoma;
KW myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.
XX
XX Homo sapiens.
OS

Key Location/Qualifiers
Peptide 1..15
FT /label= Signal_peptide
FT Protein 16..759
FT /label= Mature_protein
FT Modified-site 132..134
FT /note= "Asn is N-glycosylated"
FT Modified-site 383..385
FT /note= "Asn is N-glycosylated"
FT Modified-site 621..623
FT /note= "Asn is N-glycosylated"
FT Modified-site 631..633
FT /note= "Asn is N-glycosylated"
FT Modified-site 714..716
FT /note= "Asn is N-glycosylated"
XX
XX MO200138490-A2.
XX
XX 31-MAY-2001.
XX
XX 28-NOV-2000; 2000WO-US032403.
XX
XX 29-NOV-1999; 99US-0168151P.
XX
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX Dalla-Favera R;
XX
XX WPI; 2001-355921/37.
XX N-PSDB; AAF30950.
XX
XX New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor
PT Translocation Associated proteins, used to treat B cell malignancies
PT including lymphomas and multiple myeloma.
XX
XX Claim 3; Fig 18B-1-18B-2; 72pp; English.
XX
XX The present sequence is that of the novel human immunoglobulin receptor,
CC immunoglobulin superfamily receptor translocation associated protein
CC isoform 2a (IRTA2a), an Fc receptor involved in the pathogenesis of
CC lymphoma and melanoma. Efforts to identify genes involved in chromosomal
CC aberrations affecting band 1q21 in multiple myeloma and B cell lymphoma
CC led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding
CC members of a novel subfamily of related receptors within the

immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82314 and AAB82315). IRTA2a is a 759 amino acid secreted glycoprotein with 8 Ig-type domains followed by a unique C-terminus. IRTA2b diverges from IRTA2a at residue 560, extending for a further 32 residues. IRTA2c diverges from IRTA2a at residue 746 and extends for a further 231 residues. The IRTA genes display a specific pattern of expression in mature B cells. IRTA2 is expressed in GC centrocytes and in perifollicular cells, which may include immunoblasts and memory cells. The invention provides IRTA nucleic acids and proteins, and antibodies directed to an epitope of an IRTA protein. Methods are claimed for: detecting a B cell malignancy comprising a 1q21 chromosomal rearrangement using a nucleic acid molecule that specifically hybridises with a unique sequence of human IRTA1-5; and treating a subject having a B cell cancer by administering an anti-IRTA antibody or an antisense oligonucleotide that specifically hybridises to IRTA mRNA so as to prevent overexpression of IRTA protein and hence to arrest cell growth or induce cell death of cancer cells expressing IRTA. The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma, multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse large cell lymphoma and follicular lymphoma. The B cell lymphoma is selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-Hodgkin's lymphoma

XX
XX
SQ Sequence 759 AA;

Query Match 76.4%; Score 746; DB 4; Length 759;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLWVILLVAPVSGQARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPOKTKWYHR 60
Db 1 MLLWVILLVAPVSGQARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPOKTKWYHR 60

Qy 61 YLGEKILRETPDNIIEVQESGEYRCQAGSPLSPVHLDFFSSASLILOAPLSVFEQDSVV 120
Db 61 YLGEKILRETPDNIIEVQESGEYRCQAGSPLSPVHLDFFSSASLILOAPLSVFEQDSVV 120

Qy 121 LRCRAKAEVTLNNTIYKXNDVLAFLNKRTPHIFACLKONGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKXNDVLAFLNKRTPHIFACLKONGAYRCTGYKESCCPVSSNT 180

Qy 181 VKIQVEEFTFPVLRASSFPQISGNPVTLCETQSLERSDVPLRFRFFDDQTLGLGWS 240
Db 181 VKIQVEEFTFPVLRASSFPQISGNPVTLCETQSLERSDVPLRFRFFDDQTLGLGWS 240

Qy 241 LSPNFOITAMWSKDSGFYWCXAAITMPSVSDSPRSWIQVQIPASHVPLTSPKALNFE 300
Db 241 LSPNFOITAMWSKDSGFYWCXAAITMPSVSDSPRSWIQVQIPASHVPLTSPKALNFE 300

Qy 301 GTKVTLHCETOEDSLRTLYRFVHEGVPLRHKSVCERCASISFSLTTENSNGNYCTADNG 360
Db 301 GTKVTLHCETOEDSLRTLYRFVHEGVPLRHKSVCERCASISFSLTTENSNGNYCTADNG 360

Qy 361 LGAKPSKAVSLSVTVPSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQPHHEDAA 420
Db 361 LGAKPSKAVSLSVTVPSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQPHHEDAA 420

Qy 421 LERRANSAGGVAIFSITAEHSGNYCTADNGCPQSKAVSISITVPVSHVPLTSSA 480
Db 421 LERRANSAGGVAIFSITAEHSGNYCTADNGCPQSKAVSISITVPVSHVPLTSSA 480

Qy 481 EALTPEGATVTLHCEVQSGSPQILYQFYHEDMPLWSSSTPSVGRVSFSFSLTEGSGNYY 540
Db 481 EALTPEGATVTLHCEVQSGSPQILYQFYHEDMPLWSSSTPSVGRVSFSFSLTEGSGNYY 540

Qy 541 CTADNGFGPQREVVVSLFVTVPSRPILTLPVRAQAVVGDLELHCEAPGSPILYWF 600
Db 541 CTADNGFGPQREVVVSLFVTVPSRPILTLPVRAQAVVGDLELHCEAPGSPILYWF 600

Qy 601 YHEDVTLGSSSAPSGEASFNLSTAESHGNYSCANNGLVAQHSDDTISLSVIVPSRPI 660
Db 601 YHEDVTLGSSSAPSGEASFNLSTAESHGNYSCANNGLVAQHSDDTISLSVIVPSRPI 660

Qy 661 LTFRAPRAQAVVGDLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720
Db 661 LTFRAPRAQAVVGDLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720

Qy 721 HSGIYSCADNGLEAQRSEMVLTKVA 746
Db 721 HSGIYSCADNGLEAQRSEMVLTKVA 746

RESULT 5
ADM35235
ID ADM35235 standard; protein; 759 AA.
XX
AC ADM35235;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human LY1448P cancer related protein for cancer detection method.
XX
KW cytostatic; T-cell vaccine; detection; cancer;
KW chronic lymphocytic leukemia.
XX
OS Homo sapiens.
XX
PN WO2003077836-A2.
XX
PD 25-SEP-2003.
XX
PF 06-NOV-2002; 2002WO-US035728.
XX
PR 06-NOV-2001; 2001US-00040862.
PR 23-MAY-2002; 2002US-00154884.
XX
PA (CORI-) CORIXA CORP.
XX
PI Gaiger A, Algate PA, Mannion J, Retter M;
XX WPI; 2003-756941/71.
XX
DR Detecting cancer in a patient comprises contacting a biological sample from the patient with a binding agent that binds to a cancer-associated polypeptide and comparing the amount of polypeptide to a predetermined cutoff value.
XX
PT Disclosure; SEQ ID NO 10460; 419pp; English.
XX
PS The invention relates to a method of detecting (M1) cancer in a patient by: (i) contacting a biological sample from the patient with an agent that binds to any of three polypeptides given in the specification; (ii) detecting in a sample an amount of the peptide that binds to the binding agent; and (iii) comparing the amount of polypeptide present in the patient's sample to a predetermined cutoff value. The specification also discloses a separate method for detecting (M2) cancer in a patient by a method similar to M1, except that the detection agent is an oligonucleotide that binds to any of three polynucleotides given in the specification. M1 and M2 are useful for detecting the presence of cancer in a patient, especially chronic lymphocytic leukemia. The applicants have identified specific human polypeptides overexpressed in one or more types of hematological malignancies. This sequence corresponds to a protein used in the method of the invention.

XX
SQ Sequence 759 AA;
Query Match 76.4%; Score 746; DB 7; Length 759;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLWVILLVAPVSGQARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPOKTKWYHR 60
Db 1 MLLWVILLVAPVSGQARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPOKTKWYHR 60

Qy 61 YLGEKILRETPDNIIEVQESGEYRCQAGSPLSPVHLDFFSSASLILOAPLSVFEQDSVV 120

```
Db      61 YLKEILLRETPDNILEVQESGYRCAQGSPLSSPVHLDFSSASILLQAPLSVEFGDSVV 120
QY      121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKNDGAYRCTGYKESCCPVSSNT 180
Db      121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKNDGAYRCTGYKESCCPVSSNT 180
QY      181 VKIQVQEPPTREVLRASSFPQISGNPVTLCETQLSLERSDVPPLRFRFRDDQTLGLGWS 240
Db      181 VKIQVQEPPTREVLRASSFPQISGNPVTLCETQLSLERSDVPPLRFRFRDDQTLGLGWS 240
QY      241 LSPNFQITAMWSKDSGFYWCKAATPHSVISDSPRSWIQVOIPASHPVLTLSPEKALNFE 300
Db      241 LSPNFQITAMWSKDSGFYWCKAATPHSVISDSPRSWIQVOIPASHPVLTLSPEKALNFE 300
QY      301 GTKVLHCETQDSDRLTYRFYHEGVPLRHKSVCRCERGASISFSLTTTNSGNYCTADNG 360
Db      301 GTKVLHCETQDSDRLTYRFYHEGVPLRHKSVCRCERGASISFSLTTTNSGNYCTADNG 360
QY      361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAORGSLPILYQPHHEDAA 420
Db      361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAORGSLPILYQPHHEDAA 420
QY      421 LERRSANGAGGVAISFSLTAHSGNYYCTADNGFGPQPSKAVSLSVTPVSHPVLTLSA 480
Db      421 LERRSANGAGGVAISFSLTAHSGNYYCTADNGFGPQPSKAVSLSVTPVSHPVLTLSA 480
QY      481 EALTTEGATVTLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
Db      481 EALTTEGATVTLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
QY      541 CTADNGFGPQPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAORGSLPILYQPHHEDAA 600
Db      541 CTADNGFGPQPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAORGSLPILYQPHHEDAA 600
QY      601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTSLSVIVPVSRI 660
Db      601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTSLSVIVPVSRI 660
QY      661 LTFRAPRAQAVGDDLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT 720
Db      661 LTFRAPRAQAVGDDLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT 720
QY      721 HSGIYSCADNGLEAQRSEMTLKV 746
Db      721 HSGIYSCADNGLEAQRSEMTLKV 746
```

RESULT 6

AAB82314

ID AAB82314 standard; protein; 592 AA.

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

Query Match 57.3%; Score 560; DB 4; Length 592;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 MLWILLVLAPVSGQFARTPIIFLOPWTTPQGERVTLTKGFRFPYSPQTKWYHR 60
Db 1 MLWILLVLAPVSGQFARTPIIFLOPWTTPQGERVTLTKGFRFPYSPQTKWYHR 60
QY 61 YLKEILLRETPDNILEVQESGYRCAQGSPLSSPVHLDFSSASILLQAPLSVEFGDSVV 120
Db 61 YLKEILLRETPDNILEVQESGYRCAQGSPLSSPVHLDFSSASILLQAPLSVEFGDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKNDGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKNDGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPPTREVLRASSFPQISGNPVTLCETQLSLERSDVPPLRFRFRDDQTLGLGWS 240
Db 181 VKIQVQEPPTREVLRASSFPQISGNPVTLCETQLSLERSDVPPLRFRFRDDQTLGLGWS 240
QY 241 LSPNFQITAMWSKDSGFYWCKAATPHSVISDSPRSWIQVOIPASHPVLTLSPEKALNFE 300

Key Location/Qualifiers

Peptide 1..15

Protein 16..592

Modified-site 132..134

Modified-site 383..385

/note= "Asn is N-glycosylated"

/note= "Asn is N-glycosylated"

/note= "Asn is N-glycosylated"

/note= "Asn is N-glycosylated"

/note= "Asn is N-glycosylated"

/note= "Asn is N-glycosylated"

New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor Translocation Associated proteins, used to treat B cell malignancies including lymphomas and multiple myeloma.

Claim 3; Fig 18B-1-18B-2; 72pp; English.

The present sequence is that of the novel human immunoglobulin receptor, immunoglobulin superfamily receptor translocation associated protein isoform 2b (IRTA2b), an Fc receptor involved in the pathogenesis of lymphoma and melanoma. Efforts to identify genes involved in chromosomal aberrations affecting band 1q21 in multiple myeloma and B cell lymphoma led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding members of a novel subfamily of related receptors within the immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82314 and AAB82315). IRTA2b is a 592 amino acid glycoprotein, which diverges from IRTA2a at residue 560, extending for a further 32 residues, whose hydrophobicity suggest docking to the plasma membrane via a GPI anchor. The IRTA2 genes display a specific pattern of expression in mature B cells. IRTA2 is expressed in GC centrocytes and in perifollicular cells, which may include immunoblasts and memory cells. The invention provides IRTA nucleic acids and proteins, and antibodies directed to an epitope of an IRTA protein. Methods are claimed for: detecting a B cell malignancy comprising a 1q21 chromosomal rearrangement using a nucleic acid molecule that specifically hybridises with a unique sequence of human IRTA1-5; and treating a subject having a B cell cancer by administering an anti-IRTA antibody or an antisense oligonucleotide that specifically hybridises to IRTA mRNA so as to prevent overexpression of IRTA protein and hence to arrest cell growth or induce cell death of cancer cells expressing IRTA. The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma, multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse large cell lymphoma and follicular lymphoma. The B cell lymphoma is selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-Hodgkin's lymphoma

Sequence 592 AA;

Db 241 LSPNFQITAMWSKDSGFYWCKAATWPHSVISDSRSMIQVQIPASHPVLTLSPEKALNFE 300
Qy 301 GTKVTLHCEQEDSLRTLYRFYHEGVPLRHKSVCRCERGASISFSLTTTENSNGNYCTADNG 360
Db 301 GTKVTLHCEQEDSLRTLYRFYHEGVPLRHKSVCRCERGASISFSLTTTENSNGNYCTADNG 360
Qy 361 LCAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQPHHEDAA 420
Db 361 LCAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQPHHEDAA 420
Qy 421 LERRANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
Db 421 LERRANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
Qy 481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPVGVRVSFSLTECHSGNYY 540
Db 481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPVGVRVSFSLTECHSGNYY 540
Qy 541 CTADNGFGPQRSEVVSLEFVT 560
Db 541 CTADNGFGPQRSEVVSLEFVT 560

RESULT 7

ADM35236
ID ADM35236 standard; protein; 592 AA.

AC ADM35236;

DT 03-JUN-2004 (first entry)

DE Human LY1448P cancer related protein for cancer detection method.

Qy cytostatic; T-cell vaccine; detection; cancer;
Kw chronic lymphocytic leukemia.

XX Homo sapiens.

OS WO2003077836-A2.

PN 25-SEP-2003.

PD 06-NOV-2002; 2002WO-US035728.

PF 06-NOV-2001; 2001US-00040862.

PR 23-MAY-2002; 2002US-00154884.

XX (CORI-) CORIXA CORP.

PI Gaiger A, Algate PA, Mannion J, Retter M;

DR WPI; 2003-756941/71.

PT Detecting cancer in a patient comprises contacting a biological sample
PT from the patient with a binding agent that binds to a cancer-associated
PT polypeptide and comparing the amount of polypeptide to a predetermined
PT cutoff value.

PS Disclosure; SEQ ID NO 10461; 419pp; English.

XX The invention relates to a method of detecting (M1) cancer in a patient
CC by: (i) contacting a biological sample from the patient with an agent
CC that binds to any of three polypeptides given in the specification; (ii)
CC detecting in a sample an amount of the peptide that binds to the binding
CC agent; and (iii) comparing the amount of polypeptide present in the
CC patient's sample to a predetermined cutoff value. The specification also
CC discloses a separate method for detecting (M2) cancer in a patient by a
CC method similar to M1, except that the detection agent is an
CC oligonucleotide that binds to any of three polynucleotides given in the
CC specification. M1 and M2 are useful for detecting the presence of cancer
CC in a patient, especially chronic lymphocytic leukemia. The applicants
CC have identified specific human polypeptides overexpressed in one or more

CC types of hematological malignancies. This sequence corresponds to a
CC protein used in the method of the invention.

XX SQ Sequence 592 AA;

Query Match 57.3%; Score 560; DB 7; Length 592;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLWLWILLVLAPVSGOFARTPRPIIFLOPPWTTVFGGERVTLTCKGFRFYSQKTKWYHR 60

Db 1 MLWLWILLVLAPVSGOFARTPRPIIFLOPPWTTVFGGERVTLTCKGFRFYSQKTKWYHR 60

Qy 61 YLKEILRETPDNILEVQESGEYRCQAQGPSLSSPVHLDFSSASLIQAPLVSFEGDSVY 120

Db 61 YLKEILRETPDNILEVQESGEYRCQAQGPSLSSPVHLDFSSASLIQAPLVSFEGDSVY 120

Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHI PHACLKDNAGAYRCTGYKESCCPVSSNT 180

Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHI PHACLKDNAGAYRCTGYKESCCPVSSNT 180

Qy 181 VKIQVQEPFTRPVLRASSFPISGNPVTILTCETQLSLERSDVPFRFRDDQTGLGWS 240

Db 181 VKIQVQEPFTRPVLRASSFPISGNPVTILTCETQLSLERSDVPFRFRDDQTGLGWS 240

Qy 241 LSPNFOITAMWSKDSGFYWCKAATWPHSVISDSRSMIQVQIPASHPVLTLSPEKALNFE 300

Db 241 LSPNFOITAMWSKDSGFYWCKAATWPHSVISDSRSMIQVQIPASHPVLTLSPEKALNFE 300

Qy 301 GTKVTLHCEQEDSLRTLYRFYHEGVPLRHKSVCRCERGASISFSLTTTENSNGNYCTADNG 360

Db 301 GTKVTLHCEQEDSLRTLYRFYHEGVPLRHKSVCRCERGASISFSLTTTENSNGNYCTADNG 360

Qy 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQPHHEDAA 420

Db 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQPHHEDAA 420

Qy 421 LERRANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480

Db 421 LERRANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480

Qy 481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPVGVRVSFSLTECHSGNYY 540

Db 481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPVGVRVSFSLTECHSGNYY 540

Qy 541 CTADNGFGPQRSEVVSLEFVT 560

Db 541 CTADNGFGPQRSEVVSLEFVT 560

RESULT 8

ABP69283

ID ABP69283 standard; protein; 222 AA.

XX AC ABP69283;

XX AC 20-JAN-2003 (first entry)

DT 20-JAN-2003 (first entry)

XX Human polypeptide SEQ ID NO 1330.

XX Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW cell-proliferative disorder; neurodegenerative disease; bacterial;
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW haemostatic; vulnary; fungicide; antibacterial; virucide; protozoacide;
KW antiarthritic.

XX Homo sapiens.

XX WO200270539-A2.

XX

PD 12-SEP-2002.
 XX
 XX 05-MAR-2002; 2002WO-US005095.
 XX
 XX 05-MAR-2001; 2001US-00799451.
 XX
 XX (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
 PI Wehrman T, Wang J, Wang D, Drmanac RT;
 XX
 XX WPI: 2002-759812/82.
 DR N-PSDB; ABZ11500.
 XX
 XX New polynucleotides comprising sequences assembled from expressed
 PT sequence tags (ESTs), useful for treating cell-proliferative,
 PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
 PT or coagulation disorders.
 XX
 XX Claim 9; SEQ ID NO 1330; 1012pp + Sequence Listing; English.
 PS
 XX The invention relates to an isolated polynucleotide (I) comprising a
 CC nucleotide sequence selected from any of 948 sequences (ABZ11119-
 CC ABZ12066) or their mature protein coding portion, active domain coding
 CC protein or complementary sequences. The polynucleotides are useful for
 CC identifying expressed genes or for physical mapping of human genome. The
 CC encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
 CC markers, as a food supplement, for generating antibodies, in medical
 CC imaging, screening and diagnostic assays and for treating cell-
 CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
 CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
 CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
 CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
 CC arthritis, etc. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 222 AA;
 SQ
 Query Match 19.9%; Score 194; DB 5; Length 222;
 Best Local Similarity 100.0%; Pred. No. 1e-176;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 268 SVISDPSRWIQVQIPASHPVLTLSPEKALNFEKTKVTLHCETQEDSLRTLYRFYHEGVP 327
 DB 19 SVISDPSRWIQVQIPASHPVLTLSPEKALNFEKTKVTLHCETQEDSLRTLYRFYHEGVP 78
 QY 328 LRHKSVCBERGASISFSLTENSNGNYCTADNGLGAKPSKAVSLVTPVSHPVNLSSP 387
 DB 79 LRHKSVCBERGASISFSLTENSNGNYCTADNGLGAKPSKAVSLVTPVSHPVNLSSP 138
 QY 388 EDLIEFGAKVTTLHCAQRGSLPILYQFHEDDAALERRRANSAGGVAISFSLTAHSGNYY 447
 DB 139 EDLIEFGAKVTTLHCAQRGSLPILYQFHEDDAALERRRANSAGGVAISFSLTAHSGNYY 198
 QY 448 CTADNGFGPQRSKA 461
 DB 199 CTADNGFGPQRSKA 212
 RESULT 9
 ADE08350
 ID ADE08350 standard; protein; 268 AA.
 XX
 XX ADE08350;
 XX
 XX 29-JAN-2004 (first entry)
 XX
 XX Novel protein (useful for identifying genetic disorders) #505.
 DE novel gene; novel protein; tissue marker; molecular weight marker;
 XX
 KW

XX chromosome marker; genetic disorder.
 XX Unidentified.
 XX WO2003054152-A2.
 XX
 XX 03-JUL-2003.
 XX
 XX 10-DEC-2002; 2002WO-US039555.
 XX
 XX 10-DEC-2001; 2001US-0339739P.
 PR 11-DEC-2001; 2001US-0339453P.
 PR 14-MAR-2002; 2002US-0365091P.
 PR 14-MAR-2002; 2002US-0365384P.
 PR 12-APR-2002; 2002US-0372381P.
 PR 12-APR-2002; 2002US-0372615P.
 PR 22-APR-2002; 2002US-00128558.
 PR 24-APR-2002; 2002US-0376045P.
 XX
 XX (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
 PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
 PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
 XX
 XX WPI: 2003-569235/53.
 DR N-PSDB; ADE07439.
 XX
 XX New polynucleotides, useful for expressing recombinant proteins for
 PT analysis, characterization or therapeutic use, or as markers for tissues
 PT in which the corresponding protein is preferentially expressed.
 XX
 XX Claim 20; SEQ ID NO 1416; 1177pp; English.
 PS
 XX The invention comprises the amino acid and coding sequences of novel
 CC proteins. The DNA and protein sequences of the invention are useful as:
 CC markers for tissues in which the corresponding protein is preferentially
 CC expressed; as molecular weight markers on gels; as chromosome markers or
 CC tags; to identify chromosomes or to map related gene positions; and to
 CC compare with endogenous DNA sequences in patients to identify potential
 CC genetic disorders. The present amino acid sequence represents a protein
 CC of the invention.
 CC
 XX Sequence 268 AA;
 SQ
 Query Match 17.0%; Score 166; DB 7; Length 268;
 Best Local Similarity 100.0%; Pred. No. 8.1e-150;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 766 GDLELHCHCALRGSPILYRFFHEDVTLCNRSPSGGASLNLSTAEHSGNYSRADNGL 825
 DB 57 GDLELHCHCALRGSPILYRFFHEDVTLCNRSPSGGASLNLSTAEHSGNYSRADNGL 116
 QY 826 GAORSETVLYITGLTANRSGPFFATGVAGLLSIAGLAAGALLLYCWLRSKAGRPASDP 885
 DB 117 GAORSETVLYITGLTANRSGPFFATGVAGLLSIAGLAAGALLLYCWLRSKAGRPASDP 176
 QY 886 ARSPSPSDSQEPTVHNVPWAEELQPVYTNANRGENVYSEVRILQ 931
 DB 177 ARSPSPSDSQEPTVHNVPWAEELQPVYTNANRGENVYSEVRILQ 222
 RESULT 10
 AAY66661
 ID AAY66661 standard; protein; 124 AA.
 XX
 XX AAY66661;
 XX
 XX 05-APR-2000 (first entry)
 XX
 XX Membrane-bound protein PRO820.
 DE Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
 XX
 KW


```
XX (GETH ) GENENTECH INC.
PA Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX WPI: 2000-072883/06.
DR N-PSDB; AA264992.
XX Membrane-bound proteins and related nucleotide sequences.
PT Claim 12; Fig 83; 822pp; English.
PS The invention provides membrane-bound PRO polypeptides and
XX polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques
XX
XX Sequence 124 AA;
XX
XX Query Match 10.4%; Score 102; DB 3; Length 124;
XX Best Local Similarity 100.0%; Pred. No. 7.6e-89;
XX Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFQGERVLTCKGFRFYSPQTKWYHR 60
XX Db 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFQGERVLTCKGFRFYSPQTKWYHR 60
XX
XX QY 61 YLKGKILRETPDNILEVQESGYRCQAQGSPLSSPVHLDFFS 102
XX Db 61 YLKGKILRETPDNILEVQESGYRCQAQGSPLSSPVHLDFFS 102
XX
XX RESULT 11
XX AAB65184
XX ID AAB65184 standard; protein; 124 AA.
XX AC AAB65184;
XX DT 02-APR-2001 (first entry)
XX DE Human PRO820 (UNQ503) protein sequence SEQ ID NO:146.
XX
XX Human; secreted and transmembrane protein; PRO; cytosstatic; cell death;
XX cancer; chromosomal mapping; gene mapping; tissue typing;
XX diagnostic assay.
XX
XX OS Homo sapiens.
XX
XX FN WO200073454-A1.
XX PD 07-DEC-2000.
XX
XX PF 30-MAR-2000; 2000WO-US008439.
XX
XX PR 02-JUN-1999; 99WO-US012252.
XX PR 23-JUN-1999; 99US-0141037P.
XX PR 07-JUL-1999; 99US-0143048P.
XX PR 20-JUL-1999; 99US-0144758P.
XX PR 26-JUL-1999; 99US-0145698P.
XX PR 28-JUL-1999; 99US-0146222P.
XX PR 17-AUG-1999; 99US-0149398P.
XX PR 15-SEP-1999; 99WO-US021090.
XX
XX 15-SEP-1999; 99WO-US021547.
XX 08-OCT-1999; 99US-0158563P.
XX 30-NOV-1999; 99WO-US028313.
XX 01-DEC-1999; 99WO-US028301.
XX 16-DEC-1999; 99WO-US030095.
XX 20-DEC-1999; 99WO-US030911.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.
XX 22-FEB-2000; 2000WO-US004414.
XX 24-FEB-2000; 2000WO-US004914.
XX 02-MAR-2000; 2000WO-US005841.
XX 15-MAR-2000; 2000WO-US006884.
XX 20-MAR-2000; 2000WO-US007377.
XX
XX (GETH ) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi CJ, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;
XX Roy KA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
XX Zhang Z;
XX WPI: 2001-032160/04.
XX DR N-PSDB; AAF44138.
XX
XX PRO polynucleotides used to produce polypeptides used to target bioactive
XX molecules such as toxins, radiolabels or antibodies, to specific cells,
XX to cause targeted cell death.
XX
XX Claim 12; Fig 83; 935pp; English.
XX
XX The present invention describes human secreted and transmembrane PRO
XX proteins. The PRO proteins have cytostatic activity. The PRO proteins can
XX be used for targeted delivery of bioactive molecules, such as toxins,
XX radiolabels or antibodies, that cause cell death. PRO nucleotide
XX sequences, and their fragments, can be used as hybridisation probes, in
XX chromosomal and gene mapping, and in the generation of anti-sense RNA and
XX DNA. They may also be used to produce transgenic animals which are used
XX to develop and screen therapeutically useful reagents. The PRO nucleotide
XX and protein sequence can be used for tissue typing and in treating
XX cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
XX AAF44470 represent PCR primers and hybridisation probes used in the
XX isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
XX AAB65300 represent human PRO polynucleotide and protein sequences given
XX in the exemplification of the present invention
XX
XX Sequence 124 AA;
XX
XX Query Match 10.4%; Score 102; DB 4; Length 124;
XX Best Local Similarity 100.0%; Pred. No. 7.6e-89;
XX Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFQGERVLTCKGFRFYSPQTKWYHR 60
XX Db 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFQGERVLTCKGFRFYSPQTKWYHR 60
XX
XX QY 61 YLKGKILRETPDNILEVQESGYRCQAQGSPLSSPVHLDFFS 102
XX Db 61 YLKGKILRETPDNILEVQESGYRCQAQGSPLSSPVHLDFFS 102
XX
XX RESULT 12
XX AAB65184
XX ID AAB65184 standard; protein; 124 AA.
XX AC AAB65184;
XX DT 14-APR-2003 (first entry)
XX DE Human PRO polypeptide #31.
XX
```


XX Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
XW antibody-dependent enzyme mediated prodrug therapy.
XX
XX Homo sapiens.
OS
PN US2003027163-A1.
XX
PD 06-FEB-2003.
XX
XX 15-NOV-2001; 2001US-00997666.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 14-NOV-1997; 97US-0065710P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087753P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088739P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090245P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090355P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090472P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 24-JUN-1998; 98US-0090542P.
PR 24-JUN-1998; 98US-0090557P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 25-JUN-1998; 98US-0090698P.
PR 25-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091360P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091519P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091633P.
PR 02-JUL-1998; 98US-0091646P.
PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095285P.
PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095302P.
PR 04-AUG-1998; 98US-0095318P.
PR 04-AUG-1998; 98US-0095321P.
PR 04-AUG-1998; 98US-0095325P.
PR 10-AUG-1998; 98US-0095916P.
PR 10-AUG-1998; 98US-0095929P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.

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PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 07-OCT-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 08-JAN-1999; 99WO-US000106.
PR 08-JAN-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000375.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US020231.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.

Query Match 10.4%; Score 102; DB 6; Length 124;
Best Local Similarity 100.0%; Pred. No. 7.6e-89;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWLWLLVLAIVSGQFARTPRPIIFLOPPWTTVFQGERVLTCKGFRFYSPOKTKVHR 60
DB 1 MLWLWLLVLAIVSGQFARTPRPIIFLOPPWTTVFQGERVLTCKGFRFYSPOKTKVHR 60

QY 61 YLGKEILRTPDNILEVQSGEYRCQAQGSPLSSPVHLDFFS 102
DB 61 YLGKEILRTPDNILEVQSGEYRCQAQGSPLSSPVHLDFFS 102

RESULT 13
ABU59077
ID ABU59077 standard; protein; 124 AA.
XX
AC ABU59077;
XX
DT 28-APR-2003 (first entry)
XX
DE Novel human secreted or transmembrane protein PRO820.
XX
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW

```

KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.

XX Homo sapiens.

PN US2002132252-A1.

XX 19-SEP-2002.

XX 14-NOV-2001; 2001US-00990442.

XX 16-JUN-1997; 97US-0049787P.

PR 17-OCT-1997; 97US-0062250P.

PR 05-NOV-1997; 97WO-US020069.

PR 12-NOV-1997; 97US-0065186P.

PR 13-NOV-1997; 97US-0065311P.

PR 24-NOV-1997; 97US-0066770P.

PR 25-FEB-1998; 98US-0075945P.

PR 20-MAR-1998; 98US-0078910P.

PR 28-APR-1998; 98US-0083322P.

PR 07-MAY-1998; 98US-0084500P.

PR 28-MAY-1998; 98US-0087106P.

PR 02-JUN-1998; 98US-0087607P.

PR 02-JUN-1998; 98US-0087609P.

PR 03-JUN-1998; 98US-0087759P.

PR 04-JUN-1998; 98US-0087827P.

PR 04-JUN-1998; 98US-0088021P.

PR 04-JUN-1998; 98US-0088025P.

PR 04-JUN-1998; 98US-0088026P.

PR 04-JUN-1998; 98US-0088028P.

PR 04-JUN-1998; 98US-0088029P.

PR 04-JUN-1998; 98US-0088030P.

PR 04-JUN-1998; 98US-0088033P.

PR 05-JUN-1998; 98US-0088326P.

PR 05-JUN-1998; 98US-0088167P.

PR 05-JUN-1998; 98US-0088202P.

PR 05-JUN-1998; 98US-0088212P.

PR 05-JUN-1998; 98US-0088217P.

PR 10-JUN-1998; 98US-0088555P.

PR 10-JUN-1998; 98US-0088734P.

PR 10-JUN-1998; 98US-0088738P.

PR 10-JUN-1998; 98US-0088742P.

PR 10-JUN-1998; 98US-0088810P.

PR 10-JUN-1998; 98US-0088824P.

PR 10-JUN-1998; 98US-0088826P.

PR 11-JUN-1998; 98US-0088858P.

PR 11-JUN-1998; 98US-0088861P.

PR 11-JUN-1998; 98US-0088876P.

PR 12-JUN-1998; 98US-0089105P.

PR 16-JUN-1998; 98US-0089440P.

PR 16-JUN-1998; 98US-0089512P.

PR 16-JUN-1998; 98US-0089514P.

PR 17-JUN-1998; 98US-0089532P.

PR 17-JUN-1998; 98US-0089538P.

PR 17-JUN-1998; 98US-0089598P.

PR 17-JUN-1998; 98US-0089599P.

PR 17-JUN-1998; 98US-0089600P.

PR 17-JUN-1998; 98US-0089653P.

PR 18-JUN-1998; 98US-0089801P.

PR 18-JUN-1998; 98US-0089907P.

PR 18-JUN-1998; 98US-0089908P.

PR 18-JUN-1998; 98WO-US019330.

PR 17-SEP-1998; 98WO-US019437.

PR 07-OCT-1998; 98WO-US021141.

PR 01-DEC-1998; 98WO-US025108.

PR 05-JAN-1999; 99WO-US000106.

PR 08-MAR-1999; 99WO-US005028.

PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US000356.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023528.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
PA (GETH) GENENTECH INC.
XX
XX
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Perrara N, Fong S, Garber H, Gerritsen WE, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AJ, Kijavini IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
XX WPI; 2003-247083/24.
DR N-PSDB; ABX80219.
DE
XX
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments.
XX
XX Claim 12; Fig 83; 648pp; English.
XX
XX The invention describes an isolated human PRO polypeptide. The PRO
XX polypeptides are useful in detecting PRO polypeptides in a sample, in
XX linking a bioactive molecule to a cell expressing a PRO polypeptide, and
XX in modulating at least one biological activity of a cell expressing a PRO
XX polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
XX useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
XX stimulate adrenal cortical capillary endothelial growth, and PRO536,
XX PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
XX PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
XX useful for treating conditions or disorders where angiogenesis would be
XX beneficial, e.g. wound healing and angiogenesis of this polypeptide are
XX useful for treating cancerous tumours. PRO812 inhibits vascular
XX endothelial growth factor (VEGF) stimulated proliferation of endothelial
XX cells and is thus useful for inhibiting endothelial cell growth in
XX mammals which would be beneficial in inhibiting tumour growth. PRO826,
XX PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
XX stimulated T-lymphocytes and are therapeutically useful for enhancing
XX

CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This is the
CC amino acid sequence of a novel human PRO protein
XX
SQ Sequence 124 AA;

Query Match 10.4%; Score 102; DB 6; Length 124;
Best Local Similarity 100.0%; Pred. No. 7.6e-89;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFQGERVLTCKGFRFYSQKTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFQGERVLTCKGFRFYSQKTKWYHR 60

QY 61 YLKGKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFFS 102
DB 61 YLKGKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFFS 102

RESULT 14
ABU82589
ID ABU82589 standard; protein; 124 AA.
XX
XX AC ABU82589;
XX
XX DT 26-JUN-2003 (first entry)
XX
XX DE Human secreted/transmembrane protein PRO820.
XX
XX Human; PRO; secreted protein; transmembrane protein;
KW cardiac insufficiency disorders; angiogenesis; wound healing;
KW cancerous tumour; immune response; retinal disorder; sight loss;
KW retinitis pigmentosa; age-related macular degeneration; AMD;
KW kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;
KW Crohn's disease; sports injury; arthritis.
XX
XX OS Homo sapiens.
XX
XX US2003032023-A1.
XX
PD 13-FEB-2003.
XX
XX 14-NOV-2001; 2001US-00990711.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 02-JUN-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.

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PR	04-JUN-1998;	98US-0088030P.	PR	04-AUG-1998;	98US-0095301P.
PR	04-JUN-1998;	98US-0088033P.	PR	04-AUG-1998;	98US-0095302P.
PR	04-JUN-1998;	98US-0088032P.	PR	04-AUG-1998;	98US-0095318P.
PR	05-JUN-1998;	98US-0088167P.	PR	04-AUG-1998;	98US-0095321P.
PR	05-JUN-1998;	98US-0088202P.	PR	04-AUG-1998;	98US-0095325P.
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PR	10-JUN-1998;	98US-0088734P.	PR	11-AUG-1998;	98US-0096143P.
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PR	10-JUN-1998;	98US-0088742P.	PR	12-AUG-1998;	98US-0096329P.
PR	10-JUN-1998;	98US-0088810P.	PR	17-AUG-1998;	98US-0096757P.
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PR	12-JUN-1998;	98US-0089105P.	PR	17-AUG-1998;	98US-0096894P.
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PR	17-JUN-1998;	98US-0089598P.	PR	18-AUG-1998;	98US-0096960P.
PR	17-JUN-1998;	98US-0089599P.	PR	18-AUG-1998;	98US-0097022P.
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PR	17-JUN-1998;	98US-0089653P.	PR	20-AUG-1998;	98US-0097218P.
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PR	18-JUN-1998;	98US-0089907P.	PR	26-AUG-1998;	98US-0097952P.
PR	18-JUN-1998;	98US-0089908P.	PR	26-AUG-1998;	98US-0097954P.
PR	19-JUN-1998;	98US-0089947P.	PR	26-AUG-1998;	98US-0097955P.
PR	19-JUN-1998;	98US-0089948P.	PR	26-AUG-1998;	98US-0097971P.
PR	19-JUN-1998;	98US-0089952P.	PR	26-AUG-1998;	98US-0097978P.
PR	22-JUN-1998;	98US-0090246P.	PR	26-AUG-1998;	98US-0097979P.
PR	22-JUN-1998;	98US-0090252P.	PR	26-AUG-1998;	98US-0097986P.
PR	22-JUN-1998;	98US-0090254P.	PR	26-AUG-1998;	98US-0098014P.
PR	23-JUN-1998;	98US-0090349P.	PR	31-SEP-1998;	98US-0098525P.
PR	23-JUN-1998;	98US-0090355P.	PR	16-SEP-1998;	98US-0100634P.
PR	24-JUN-1998;	98US-0090429P.	PR	16-SEP-1998;	98US-0100634P.
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PR	24-JUN-1998;	98US-0090445P.	PR	07-OCT-1998;	98US-0100858P.
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PR	24-JUN-1998;	98US-0090540P.	PR	05-JAN-1999;	98US-0113296P.
PR	24-JUN-1998;	98US-0090557P.	PR	08-MAR-1999;	98US-0113296P.
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PR	01-JUL-1998;	98US-0091544P.	PR	08-OCT-1999;	98US-0158663P.
PR	02-JUL-1998;	98US-0091478P.	PR	30-NOV-1999;	98US-0158663P.
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PR	02-JUL-1998;	98US-0091626P.	PR	01-DEC-1999;	98US-0158663P.
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PR	02-JUL-1998;	98US-0091673P.	PR	05-JAN-2000;	98US-0158663P.
PR	07-JUL-1998;	98US-0091982P.	PR	06-JAN-2000;	98US-0158663P.
PR	09-JUL-1998;	98US-0092182P.	PR	11-FEB-2000;	98US-0158663P.
PR	10-JUL-1998;	98US-0092472P.	PR	18-FEB-2000;	98US-0158663P.
PR	20-JUL-1998;	98US-0093339P.	PR	24-FEB-2000;	98US-0158663P.
PR	30-JUL-1998;	98US-0094651P.	PR	24-FEB-2000;	98US-0158663P.
PR	04-AUG-1998;	98US-0095282P.	PR	02-MAR-2000;	98US-0158663P.
PR	04-AUG-1998;	98US-0095285P.	PR	10-MAR-2000;	98US-0158663P.

PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US030710.
PR 11-AUG-2000; 2000WO-US022031.

Query Match 10.4%; Score 102; DB 6; Length 124;

Best Local Similarity 100.0%; Pred. No. 7.6e-89; Mismatches 0; Indels 0; Gaps 0;

Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB |||||
1 MLWLWILLIAPVSGQFARTPRPIIFLOPPWTVFGQGVTLTKGFRFYSPQKTWYHR 60

QY 61 YLKGKILRETPNILEVQSGEYRCQAQGSPLSSPVHLDFFS 102

DB |||||
61 YLKGKILRETPNILEVQSGEYRCQAQGSPLSSPVHLDFFS 102

RESULT 15

ABU60508

ID ABU60508 standard; protein; 124 AA.

XX AC ABU60508;

XX DT 01-MAY-2003 (first entry)

XX DE Human secreted/transmembrane protein, #52.

XX KW Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical;

XX KW diagnostic; therapeutic; Gene therapy.

XX OS Homo sapiens.

XX PN US2002160384-A1.

XX PD 31-OCT-2002.

XX PF 14-NOV-2001; 2001US-0092529S.

XX 16-JUN-1997; 97US-0049787P.

PR 17-OCT-1997; 97US-0062250P.

PR 05-NOV-1997; 97WO-US020069.

PR 12-NOV-1997; 97US-0065186P.

PR 13-NOV-1997; 97US-0065311P.

PR 24-NOV-1997; 97US-0066770P.

PR 25-FEB-1998; 98US-0075945P.

PR 20-MAR-1998; 98US-0078910P.

PR 28-APR-1998; 98US-0083322P.

PR 07-MAY-1998; 98US-0084600P.

PR 28-MAY-1998; 98US-0087106P.

PR 02-JUN-1998; 98US-0087607P.

PR 02-JUN-1998; 98US-0087609P.

PR 02-JUN-1998; 98US-0087759P.

PR 03-JUN-1998; 98US-0087827P.

PR 04-JUN-1998; 98US-0088021P.

PR 04-JUN-1998; 98US-0088025P.

PR 04-JUN-1998; 98US-0088026P.

PR 04-JUN-1998; 98US-0088028P.

PR 04-JUN-1998; 98US-0088029P.

PR 04-JUN-1998; 98US-0088030P.

PR 04-JUN-1998; 98US-0088033P.

PR 04-JUN-1998; 98US-0088036P.

PR 05-JUN-1998; 98US-0088167P.

PR 05-JUN-1998; 98US-0088202P.

PR 05-JUN-1998; 98US-0088212P.

PR 05-JUN-1998; 98US-0088217P.

PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
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PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 18-JUN-1998; 98US-0089933P.
PR 18-JUN-1998; 98US-0089933P.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 98WO-US005028.
PR 02-JUN-1999; 98WO-US012252.
PR 15-SEP-1999; 98WO-US021090.
PR 15-SEP-1999; 98WO-US021547.
PR 30-NOV-1999; 98WO-US028313.
PR 01-DEC-1999; 98WO-US028301.
PR 01-DEC-1999; 98WO-US028634.
PR 16-DEC-1999; 98WO-US030095.
PR 20-DEC-1999; 98WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US019692.
PR 09-JUL-2001; 2001WO-US021066.
PR 28-AUG-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001WO-US0341992.

(GETH) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tamas D, Watanabe CK, Williams PM, Wood WI;

PI Zhang Z;
XX
DR WPI; 2003-288106/28.
DR N-PSDB; ABX90197.
XX
PT New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
PT chromosome markers, or in generating probes.
XX
XX
PS Claim 12; Fig 83; 650pp; English.
XX
CC The invention discloses isolated PRO secreted/transmembrane polypeptides
CC comprising a sequence without signal peptide and the nucleic acid
CC encoding them. The polypeptides can be used to raise antibodies that
CC specifically bind to the PRO polypeptide, for linking a bioactive
CC molecule to a cell expressing a PRO protein and for modulating at least
CC one biological activity of a cell. The PRO polypeptides or
CC polynucleotides are also useful in gene therapy, in chromosome
CC identification, as chromosome markers, or in generating probes. The PRO
CC polypeptides are useful as molecular markers for protein electrophoresis,
CC and the isolated nucleic acids may be used for recombinantly expressing
CC those markers. The PRO polypeptides and nucleic acids may also be used in
CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
CC PRO, and in affinity purification of PRO from recombinant cell culture or
CC natural sources. The sequences presented in AB060478-AB060624 are the PRO
CC polynucleotides of the invention. Note: The sequence data for this patent
CC is also available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 124 AA;

Query Match 10.4%; Score 102; DB 6; Length 124;
Best Local Similarity 100.0%; Pred. No. 7.6e-89;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db |||||||
QY 1 MLLWVLLVLPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPQTKWYHR 60
Db |||||||
QY 61 YLKGKILRETPDNILEVQSGEYRCAQGSPLSSPVHLDFFS 102
Db |||||||
QY 61 YLKGKILRETPDNILEVQSGEYRCAQGSPLSSPVHLDFFS 102
Db |||||||

Search completed: November 18, 2004, 13:01:27
Job time : 166 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2004, 13:05:09 ; Search time 155 Seconds

(without alignments)
2232.146 Million cell updates/sec

Title: US-09-724-254A-41

Perfect score: 977
Sequence: 1 MLLWVILLVLPVSGQFART.....KVASTPVSGSLFIASSAPHR 977

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1570615 seqs, 354127592 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	977	100.0	977	14	US-10-040-862-10462 Sequence 10462, A
2	977	100.0	977	15	US-10-057-475B-10461 Sequence 10462, A
3	977	100.0	977	15	US-10-154-884B-10462 Sequence 10462, A
4	977	100.0	977	15	US-10-403-847-9 Sequence 9, Appli
5	977	100.0	977	16	US-10-764-324-10462 Sequence 10462, A
6	788	80.7	977	14	US-10-241-220-97 Sequence 97, Appl
7	746	76.4	759	14	US-10-040-862-10460 Sequence 10460, A
8	746	76.4	759	15	US-10-057-475B-10460 Sequence 10460, A
9	746	76.4	759	15	US-10-154-884B-10460 Sequence 10460, A
10	746	76.4	759	15	US-10-403-847-7 Sequence 7, Appli
11	746	76.4	759	16	US-10-764-324-10460 Sequence 10460, A
12	644	65.9	790	15	US-10-403-847-4 Sequence 4, Appli
13	560	57.3	592	14	US-10-040-862-10461 Sequence 10461, A

14	560	57.3	592	15	US-10-057-475B-10461	Sequence 10461, A
15	560	57.3	592	15	US-10-154-884B-10461	Sequence 10461, A
16	560	57.3	592	15	US-10-403-847-8	Sequence 8, Appli
17	560	57.3	592	16	US-10-764-324-10461	Sequence 10461, A
18	281	28.8	317	15	US-10-403-847-2	Sequence 2, Appli
19	246	25.2	438	15	US-10-403-847-6	Sequence 6, Appli
20	151	15.5	152	15	US-10-403-847-10	Sequence 10, Appli
21	113	11.6	113	15	US-10-403-847-139	Sequence 139, App
22	102	10.4	102	15	US-10-403-847-124	Sequence 124, App
23	102	10.4	124	9	US-09-989-723-146	Sequence 146, App
24	102	10.4	124	9	US-09-989-723-146	Sequence 146, App
25	102	10.4	124	9	US-09-989-273-146	Sequence 146, App
26	102	10.4	124	9	US-09-989-727-146	Sequence 146, App
27	102	10.4	124	9	US-09-989-731-146	Sequence 146, App
28	102	10.4	124	9	US-09-989-732-146	Sequence 146, App
29	102	10.4	124	9	US-09-991-073-146	Sequence 146, App
30	102	10.4	124	9	US-09-990-443-146	Sequence 146, App
31	102	10.4	124	9	US-09-991-163-146	Sequence 146, App
32	102	10.4	124	9	US-09-993-604-146	Sequence 146, App
33	102	10.4	124	9	US-09-990-456-146	Sequence 146, App
34	102	10.4	124	9	US-09-989-721-146	Sequence 146, App
35	102	10.4	124	9	US-09-992-598-146	Sequence 146, App
36	102	10.4	124	9	US-09-989-293A-146	Sequence 146, App
37	102	10.4	124	9	US-09-989-735-146	Sequence 146, App
38	102	10.4	124	9	US-09-990-444-146	Sequence 146, App
39	102	10.4	124	9	US-09-991-181-146	Sequence 146, App
40	102	10.4	124	9	US-09-989-730-146	Sequence 146, App
41	102	10.4	124	9	US-09-990-436-146	Sequence 146, App
42	102	10.4	124	9	US-09-993-687-146	Sequence 146, App
43	102	10.4	124	10	US-09-989-734-146	Sequence 146, App
44	102	10.4	124	10	US-09-997-653-146	Sequence 146, App
45	102	10.4	124	10	US-09-989-724-146	Sequence 146, App

ALIGNMENTS

RESULT 1

US-10-040-862-10462
; Sequence 10462, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416

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; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10462
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-10462

Query Match      100.0%; Score 977; DB 14; Length 977;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLLWVILLVAPVSGGFARTPRPIIFLOPPWTTVFGGERVTLTCKGFRFYSPQKTWYHR 60

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Db 121 LCRKAETVLTNTIYKNDNVLAFLNKRTDPIHACLDKNGAYRCTGYKSCCPVSSNT 180

Qy 181 VKIQVEPTRPVLRASSQPIISGNPVTLCETQSLERSDVPVLRFRFRDDQTLGLWS 240
Db 181 VKIQVEPTRPVLRASSQPIISGNPVTLCETQSLERSDVPVLRFRFRDDQTLGLWS 240

Qy 241 LSPNFOITAWKSDGFYWCXKATMPHSVISDSPSWIQVOIPASHPVLTLSPEKALNFE 300
Db 241 LSPNFOITAWKSDGFYWCXKATMPHSVISDSPSWIQVOIPASHPVLTLSPEKALNFE 300

Qy 301 GTKVTLHCETQDSLTLYRFYHGVPLRHKSVRCERGASISFSLTTSNGNYCTADNG 360
Db 301 GTKVTLHCETQDSLTLYRFYHGVPLRHKSVRCERGASISFSLTTSNGNYCTADNG 360

Qy 361 LGAKSKAVSLSVTVPSHPVNLSPEDLIFEGAKVTLHCEAQRGSPIIYQHHEDAA 420
Db 361 LGAKSKAVSLSVTVPSHPVNLSPEDLIFEGAKVTLHCEAQRGSPIIYQHHEDAA 420

Qy 421 LRRSANSAGGVAISFSLTAHSGNYCYCTADNGFGPQRSKAVSLIIVPSHPVLTLSA 480
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961 STPVSGSLFIASSAPHR 977
961 STPVSGSLFIASSAPHR 977

RESULT 2
US-10-057-475B-10462
; Sequence 10462, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aljun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10462
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-10462

Query Match      100.0%; Score 977; DB 15; Length 977;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 YLGEKILRETPDNILVQESGVRCAQGSPLSSPVHLDFSSASLILOAPLSVFEQSVV 120
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Db 841 TANRSGPFATGVAGGLLSTAGLAAGALLLYCWLRSKAGRKPAASDPARSFSDSDSQEPTYH 900
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QY 961 STPVSGSLFLASSAPHR 977
Db 961 STPVSGSLFLASSAPHR 977

RESULT 4

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; Sequence 9, Application US/10403847
; Publication No. US20040030098A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLICED VARIANTS OF A HUMAN
; FILE REFERENCE: D0228 NP
; CURRENT APPLICATION NUMBER: US/10/403,847
; PRIOR FILING DATE: 2003-03-28
; PRIOR FILING DATE: 2002-03-29
; PRIOR FILING DATE: 2002-03-29
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-847-9

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 YLCKEILRETPDNILEVOESGEYRCAQSPSSPVHLDFFSSASLIQAPLSVFEGDSVY 120
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Db 121 LRCRAAEVTLNNTIYKNDNVLAFLNKRDTFPHIACLDKNGAYRGTGKESCCPVSSNT 180
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Db 241 LSNFQITAMWSKDSGFYWKCAATMPHSVSDSPRSWIOVQIPASHPVLTLSPEKALNPE 300
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Db 421 LERRANSAGGVAISFSLTAHSGNYSCTADNGFGPORSKAVSLSTVPSHPVLTLSA 480
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Db 481 EALTTFEGATVTLHCEVQORSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEHSGNY 540
QY 541 CTADNGFGPORSSEVSLFVTVPVSRPILTLRVPRAQAVVGDLLLEHCEAPRGSPPILYWF 600
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Db 601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPSRPI 660
QY 661 LTFRAPRAQAVVGDLLLEHCEALRGSSPILYFYHEDVTLGKISAPSGGGASFNLSLTTE 720
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Db 721 HSGIYSCDADNGLEAQRSEMTLKVAVPVSRPILTLRPAQTHAAVGDLLLEHCEALRGSP 780
QY 781 LILYRFFHEDVTLGNRSSPSGGASLNLSTAEHSGNYSCEANGLVAQHSDDTISLSVIVPSRPI 840
Db 781 LILYRFFHEDVTLGNRSSPSGGASLNLSTAEHSGNYSCEANGLVAQHSDDTISLSVIVPSRPI 840
QY 841 TANRSGPFATGVAGGLLSTAGLAAGALLLYCWLRSKAGRKPAASDPARSFSDSDSQEPTYH 900
Db 841 TANRSGPFATGVAGGLLSTAGLAAGALLLYCWLRSKAGRKPAASDPARSFSDSDSQEPTYH 900
QY 901 NVPAAEELQPVYTNANPRGENVYSEVRITIQEKKHAAVADDPHRLNKGSPPIIYSEVKVA 960
Db 901 NVPAAEELQPVYTNANPRGENVYSEVRITIQEKKHAAVADDPHRLNKGSPPIIYSEVKVA 960
QY 961 STPVSGSLFLASSAPHR 977
Db 961 STPVSGSLFLASSAPHR 977

RESULT 5

US-10-764-324-10462
; Sequence 10462, Application US/10764324
; Publication No. US2004017579A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/764,324
; CURRENT FILING DATE: 2004-01-23
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126

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; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10462
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-324-10462

Query Match
Best Local Similarity 100.0%; Score 977; DB 16; Length 977;
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSQKTKWYHR 60
DB 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSQKTKWYHR 60

QY 61 YLGEILRETPDNILEVQESGEYRQCAQGSPLSSPVHLDFSSASLILOAPLSVFEQSVV 120
DB 61 YLGEILRETPDNILEVQESGEYRQCAQGSPLSSPVHLDFSSASLILOAPLSVFEQSVV 120

QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHPHACLKDNKAYRGTCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHPHACLKDNKAYRGTCTGYKESCCPVSSNT 180

QY 181 VKIQVEPFTPRVLRASSFQISGNPVTTCETQSLERSDVPFRFRDQTLGLGWS 240
DB 181 VKIQVEPFTPRVLRASSFQISGNPVTTCETQSLERSDVPFRFRDQTLGLGWS 240

QY 241 LSPNFOITAMWSKDSGFYWCACKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKALNFE 300
DB 241 LSPNFOITAMWSKDSGFYWCACKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKALNFE 300

QY 301 GTKVTLHCETQDSLTURLTYRFYHGVPLRHKSVCRCERGASISFSLTTTENSNGNYCTADNG 360
DB 301 GTKVTLHCETQDSLTURLTYRFYHGVPLRHKSVCRCERGASISFSLTTTENSNGNYCTADNG 360

QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPDLIPEGAKVTLHCEAQRGSLPILOQFHHDDAA 420
DB 361 LGAKPSKAVSLSVTPVSHPVNLSSPDLIPEGAKVTLHCEAQRGSLPILOQFHHDDAA 420

QY 421 LERRSANGAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
DB 421 LERRSANGAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480

QY 481 EALTTEGATVTLHCEVQRGSPQILYQFVHEDMPLWSSSTPSVGRVSFSLTEHSGNY 540
DB 481 EALTTEGATVTLHCEVQRGSPQILYQFVHEDMPLWSSSTPSVGRVSFSLTEHSGNY 540

QY 541 CTADNGFGPQRSEVSVLFTVTPVSRPIILTRVPRQAQVVGDLLELHCEAPRGSPPILYWF 600
DB 541 CTADNGFGPQRSEVSVLFTVTPVSRPIILTRVPRQAQVVGDLLELHCEAPRGSPPILYWF 600

QY 601 YHEDVTLGSSSAPSGCEASFNLSLTAHSGNYSCANNGLVAQHSDDTISLSVIVPVSRI 660
DB 601 YHEDVTLGSSSAPSGCEASFNLSLTAHSGNYSCANNGLVAQHSDDTISLSVIVPVSRI 660
```

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661 LTRAPRAQAVVGDILLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLITE 720
661 LTRAPRAQAVVGDILLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLITE 720
721 HSGIYSCADNGLEAQRSEMWTLKVAVPVSRPVLTLRAPGTHAAVGDILLELHCEALRGSP 780
721 HSGIYSCADNGLEAQRSEMWTLKVAVPVSRPVLTLRAPGTHAAVGDILLELHCEALRGSP 780
781 LILYRFHEDVTLGNRSSPSSGGASLNLSTAHSGNYSCADNGLGAQRSEVTLITGL 840
781 LILYRFHEDVTLGNRSSPSSGGASLNLSTAHSGNYSCADNGLGAQRSEVTLITGL 840
841 TANRSGPFATGVAGGLLSIAGLAAGALLLYCWLRSKAGRPASDPARSPSDSDSQBPYTH 900
841 TANRSGPFATGVAGGLLSIAGLAAGALLLYCWLRSKAGRPASDPARSPSDSDSQBPYTH 900
901 NVPABEELQPVYTNANPRGENVYSEVRIIOEKKKHAVASDPRLRNKKGSPPIYSEVKVA 960
901 NVPABEELQPVYTNANPRGENVYSEVRIIOEKKKHAVASDPRLRNKKGSPPIYSEVKVA 960
961 STPVSGSLFLASSAPHR 977
961 STPVSGSLFLASSAPHR 977

RESULT 6
US-10-241-220-97
; Sequence 97, Application US/10241220
; Publication No. US20030148408A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5010R1-US
; CURRENT APPLICATION NUMBER: US/10/241,220
; CURRENT FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 97
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-241-220-97

Query Match
Best Local Similarity 80.7%; Score 788; DB 14; Length 977;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 888; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSQKTKWYHR 60
DB 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSQKTKWYHR 60

QY 61 YLGEILRETPDNILEVQESGEYRQCAQGSPLSSPVHLDFSSASLILOAPLSVFEQSVV 120
DB 61 YLGEILRETPDNILEVQESGEYRQCAQGSPLSSPVHLDFSSASLILOAPLSVFEQSVV 120

QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHPHACLKDNKAYRGTCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHPHACLKDNKAYRGTCTGYKESCCPVSSNT 180

QY 181 VKIQVEPFTPRVLRASSFQISGNPVTTCETQSLERSDVPFRFRDQTLGLGWS 240
DB 181 VKIQVEPFTPRVLRASSFQISGNPVTTCETQSLERSDVPFRFRDQTLGLGWS 240

QY 241 LSPNFOITAMWSKDSGFYWCACKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKALNFE 300
DB 241 LSPNFOITAMWSKDSGFYWCACKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKALNFE 300
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Db 241 LSPNFOITAMWSKDSGFYWCKAATMPHSVSDSPRSWQVQIPASHPVLTLSPEKALNFE 300
 Qy 301 GTKVTLHCETQEDSLTLRYFHEGVPLHKSVCERGASISFSLTTTENSNGNYCTADNG 360
 Db 301 GTKVTLHCETQEDSLTLRYFHEGVPLHKSVCERGASISFSLTTTENSNGNYCTADNG 360
 Qy 361 LGAKPKSAVSLSVTPVSHPVNLSPEDLIFEGAKVTLHCEAQRGSPIPLYQFHEDAA 420
 Db 361 LGAKPKSAVSLSVTPVSHPVNLSPEDLIFEGAKVTLHCEAQRGSPIPLYQFHEDAA 420
 Qy 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLITVPSHPVLTLSA 480
 Db 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLITVPSHPVLTLSA 480
 Qy 481 EALTFFEGATVTLHCEVQRGSPQLYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGNY 540
 Db 481 EALTFFEGATVTLHCEVQRGSPQLYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGNY 540
 Qy 541 CTADNGFGPQRSEVSLFVTVPVSRPILTLRVPRAQAVVGDLLHCEAPRGSPPILYWF 600
 Db 541 CTADNGFGPQRSEVSLFVTVPVSRPILTLRVPRAQAVVGDLLHCEAPRGSPPILYWF 600
 Qy 601 YHEDVTLGSSSAPSGGEAFSNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPSRPI 660
 Db 601 YHEDVTLGSSSAPSGGEAFSNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPSRPI 660
 Qy 661 LTFRAPRAQAVVGDLLHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720
 Db 661 LTFRAPRAQAVVGDLLHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720
 Qy 721 HSGIYSCDADNGLEAQRSEMTLVKAVPVSRPILRAPGTHAAVGDLLHCEALRGSP 780
 Db 721 HSGIYSCDADNGLEAQRSEMTLVKAVPVSRPILRAPGTHAAVGDLLHCEALRGSP 780
 Qy 781 LILYRFHEDVTLGSRSSPGGASNLTLTAHSGNYSCEADNGLGAQRSETVLIYITGL 840
 Db 781 LILYRFHEDVTLGSRSSPGGASNLTLTAHSGNYSCEADNGLGAQRSETVLIYITGL 840
 Qy 841 TANRSGPPTAGVAGGLLSIAGLAAGALLLYCWLRSKAGRKPADSPARSP 889
 Db 841 TANRSGPPTAGVAGGLLSIAGLAAGALLLYCWLRSKAGRKPADSPARSP 889

RESULT 7
 US-10-040-862-10460
 ; Sequence 10460, Application US/10040862
 ; Publication No. US20030078396A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Algate, Paul A.
 ; APPLICANT: Wannion, Jane
 ; APPLICANT: Retter, Marc
 ; APPLICANT: Corixa Corporation
 ; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
 ; TITLE OF INVENTION: Hematological Malignancies
 ; FILE REFERENCE: 014058-013520US
 ; CURRENT APPLICATION NUMBER: US/10/040, 862
 ; CURRENT FILING DATE: 2001-11-06
 ; PRIOR APPLICATION NUMBER: US 60/186,126
 ; PRIOR FILING DATE: 2000-03-01
 ; PRIOR APPLICATION NUMBER: US 60/190,479
 ; PRIOR FILING DATE: 2000-03-17
 ; PRIOR APPLICATION NUMBER: US 60/200,545
 ; PRIOR FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: US 60/200,303
 ; PRIOR FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: US 60/200,779
 ; PRIOR FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: US 60/200,999
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: US 60/202,084
 ; PRIOR FILING DATE: 2000-05-04
 ; PRIOR APPLICATION NUMBER: US 60/206,201

; PRIOR FILING DATE: 2000-05-22
 ; PRIOR APPLICATION NUMBER: US 60/218,950
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: US 60/222,903
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: US 60/223,416
 ; PRIOR FILING DATE: 2000-08-04
 ; PRIOR APPLICATION NUMBER: US 60/223,378
 ; PRIOR FILING DATE: 2000-08-07
 ; PRIOR APPLICATION NUMBER: US 09/796,692
 ; PRIOR FILING DATE: 2001-03-01
 ; NUMBER OF SEQ ID NOS: 10467
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 10460
 ; LENGTH: 759
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-040-862-10460

Query Match 76.4%; Score 746; DB 14; Length 759;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLWVILLVLPVSGOFARTPREIIFLOPPWTTVFOGERVTLTKGFRFYSQKTKWYR 60
 Db 1 MLLWVILLVLPVSGOFARTPREIIFLOPPWTTVFOGERVTLTKGFRFYSQKTKWYR 60
 Qy 61 YLGEKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFFSSASLILQAPLSVFEGDSVY 120
 Db 61 YLGEKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFFSSASLILQAPLSVFEGDSVY 120
 Qy 121 LRCRAKAEVTLNNTIYKNDNLVAFLNKRTDFHIFHACILKONGAYRCTGKYKSCCPVSSNT 180
 Db 121 LRCRAKAEVTLNNTIYKNDNLVAFLNKRTDFHIFHACILKONGAYRCTGKYKSCCPVSSNT 180
 Qy 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLTCTQLSLERSDVPLFRFRFRDDQTLGLWS 240
 Db 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLTCTQLSLERSDVPLFRFRFRDDQTLGLWS 240
 Qy 241 LSNFOITAMWSKDSGFYWCKAATMPHSVSDSPRSWQVQIPASHPVLTLSPEKALNFE 300
 Db 241 LSNFOITAMWSKDSGFYWCKAATMPHSVSDSPRSWQVQIPASHPVLTLSPEKALNFE 300
 Qy 301 GTKVTLHCETQEDSLTLRYFHEGVPLHKSVCERGASISFSLTTTENSNGNYCTADNG 360
 Db 301 GTKVTLHCETQEDSLTLRYFHEGVPLHKSVCERGASISFSLTTTENSNGNYCTADNG 360
 Qy 361 LGAKPKSAVSLSVTPVSHPVNLSPEDLIFEGAKVTLHCEAQRGSPIPLYQFHEDAA 420
 Db 361 LGAKPKSAVSLSVTPVSHPVNLSPEDLIFEGAKVTLHCEAQRGSPIPLYQFHEDAA 420
 Qy 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLITVPSHPVLTLSA 480
 Db 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLITVPSHPVLTLSA 480
 Qy 481 EALTFFEGATVTLHCEVQRGSPQLYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGNY 540
 Db 481 EALTFFEGATVTLHCEVQRGSPQLYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGNY 540
 Qy 541 CTADNGFGPQRSEVSLFVTVPVSRPILTLRVPRAQAVVGDLLHCEAPRGSPPILYWF 600
 Db 541 CTADNGFGPQRSEVSLFVTVPVSRPILTLRVPRAQAVVGDLLHCEAPRGSPPILYWF 600
 Qy 601 YHEDVTLGSSSAPSGGEAFSNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPSRPI 660
 Db 601 YHEDVTLGSSSAPSGGEAFSNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPSRPI 660
 Qy 661 LTFRAPRAQAVVGDLLHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720
 Db 661 LTFRAPRAQAVVGDLLHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720
 Qy 721 HSGIYSCDADNGLEAQRSEMTLVKVA 746

Db 721 HSGIYSCDADNGLEAQRSEWTLKVA 746

RESULT 8

US-10-057-475B-10460

; Sequence 10460, Application US/10057475B

; Publication No. US20040002068A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Mannion, Paul A.

; APPLICANT: Clapper, Jonathan David

; APPLICANT: Wang, Aijun

; APPLICANT: Ordenez, Nadia

; APPLICANT: Carter, Lauren

; APPLICANT: McNeill, Patricia Dianne

; APPLICANT: Corixa Corporation

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

; TITLE OF INVENTION: Hematological Malignancies

; FILE REFERENCE: 014058-014402US

; CURRENT APPLICATION NUMBER: US/10/057,475B

; CURRENT FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: US 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: US 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: US 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: US 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,779

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,999

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: US 60/202,084

; PRIOR FILING DATE: 2000-05-04

; PRIOR APPLICATION NUMBER: US 60/206,201

; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: US 60/218,950

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 60/222,903

; PRIOR FILING DATE: 2000-08-03

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 10979

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 10460

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-057-475B-10460

Query Match 76.4%; Score 746; DB 15; Length 759;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLWILLVAPVSGQFARTPRPIIFLOPPWTVFGGERVITCKGFRFYSFQKTKWYHR 60

Db 1 MLLWILLVAPVSGQFARTPRPIIFLOPPWTVFGGERVITCKGFRFYSFQKTKWYHR 60

Qy 61 YLGKILRETPDNILEVQESGYRCQAGSPLSSVHLDFSSASLILQAPLSVFEQDSVW 120

Db 61 YLGKILRETPDNILEVQESGYRCQAGSPLSSVHLDFSSASLILQAPLSVFEQDSVW 120

Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTFHI PHACLKDNAGYACTGYKSCCPVSSNT 180

Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTFHI PHACLKDNAGYACTGYKSCCPVSSNT 180

Qy 181 VKIQVQEPTRPVLRASSQPIISGNPVTITCTQSLERSDVPLFRFRDDQTLGLGWS 240

Db 181 VKIQVQEPTRPVLRASSQPIISGNPVTITCTQSLERSDVPLFRFRDDQTLGLGWS 240

Qy 241 LSPNFQITAMWSKDSGFYWKCAATMPHSVISDSPRSWIQVQIPASHPVLTLSPEKALNFE 300

Db 241 LSPNFQITAMWSKDSGFYWKCAATMPHSVISDSPRSWIQVQIPASHPVLTLSPEKALNFE 300

Qy 301 GTKVTLHCETOEDSLRTLYRFYHEGVPLRHKSVCERGASISFSLTTEGSGNYCTADNG 360

Db 301 GTKVTLHCETOEDSLRTLYRFYHEGVPLRHKSVCERGASISFSLTTEGSGNYCTADNG 360

Qy 361 LGAKPSKAVSLSVTPVSHPVNLNLSPPDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420

Db 361 LGAKPSKAVSLSVTPVSHPVNLNLSPPDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420

Qy 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSTVPVSHPVLTLSA 480

Db 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSTVPVSHPVLTLSA 480

Qy 481 EALTTEGATVTLHCEYQGRSPQILYQFYHEDMPLWSSSTPSYGRVSFSLTEGSGNY 540

Db 481 EALTTEGATVTLHCEYQGRSPQILYQFYHEDMPLWSSSTPSYGRVSFSLTEGSGNY 540

Qy 541 CTADNGFGPORSSEVSLFTVTVPSRILTLRVPRQAVVGDLELHCEAPRSPPILYWF 600

Db 541 CTADNGFGPORSSEVSLFTVTVPSRILTLRVPRQAVVGDLELHCEAPRSPPILYWF 600

Qy 601 YHEDVTLGSSSAPSGGGEASFNLSTLTAHSGNYSCGANGLVAQHSDTISLSVIVPVSRI 660

Db 601 YHEDVTLGSSSAPSGGGEASFNLSTLTAHSGNYSCGANGLVAQHSDTISLSVIVPVSRI 660

Qy 661 LTFRPRQAVVGDLELHCEALRGSSPILYQFYHEDVTLGKISAPSGGASFNLSLTTE 720

Db 661 LTFRPRQAVVGDLELHCEALRGSSPILYQFYHEDVTLGKISAPSGGASFNLSLTTE 720

Qy 721 HSGIYSCDADNGLEAQRSEWTLKVA 746

Db 721 HSGIYSCDADNGLEAQRSEWTLKVA 746

RESULT 9

US-10-154-884B-10460

; Sequence 10460, Application US/10154884B

; Publication No. US20040005561A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; APPLICANT: Retter, Marc W.

; APPLICANT: Corixa Corporation

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

; TITLE OF INVENTION: Hematological Malignancies

; FILE REFERENCE: 014058-013521US

; CURRENT APPLICATION NUMBER: US/10/154,884B

; CURRENT FILING DATE: 2002-05-23

; PRIOR APPLICATION NUMBER: US 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: US 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: US 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: US 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,779

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,999

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: US 60/202,084

; PRIOR FILING DATE: 2000-05-04

; PRIOR APPLICATION NUMBER: US 60/206,201

; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: US 60/218,950

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 60/222,903

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 11290

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 10460
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-10460

Query Match 76.4%; Score 746; DB 15; Length 759;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MLLWVILLVLPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTKGFRFYSPOKTKWYHR	60
DB	1	MLLWVILLVLPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTKGFRFYSPOKTKWYHR	60
QY	61	YLKKEILRETPDNILVQSGEYRCQAQSPSSPVHLDFFSSASLILOAPLSVFEQDSVV	120
DB	61	YLKKEILRETPDNILVQSGEYRCQAQSPSSPVHLDFFSSASLILOAPLSVFEQDSVV	120
QY	121	LCRAKAEVTLNNTIYKNDNVLAFLNKRDPHIFACLDKNGAYRCTGYKESCCPVSSNT	180
DB	121	LCRAKAEVTLNNTIYKNDNVLAFLNKRDPHIFACLDKNGAYRCTGYKESCCPVSSNT	180
QY	181	VKIQVEPTPRVLRASSQPIISGNPVTCTQTSLSERSDVLPRFRDDQTLGLGWS	240
DB	181	VKIQVEPTPRVLRASSQPIISGNPVTCTQTSLSERSDVLPRFRDDQTLGLGWS	240
QY	241	LSNFOITAMWSDSGFYWCKAATMPHSVISDSPRSWIQVQIPASHPVLTLSPEKALNFE	300
DB	241	LSNFOITAMWSDSGFYWCKAATMPHSVISDSPRSWIQVQIPASHPVLTLSPEKALNFE	300
QY	301	GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCRCERGASISFSLTNSGNYCTADNG	360
DB	301	GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCRCERGASISFSLTNSGNYCTADNG	360
QY	361	LGAKPSKAVSLSVTVPSHPVLNLSPPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA	420
DB	361	LGAKPSKAVSLSVTVPSHPVLNLSPPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA	420
QY	421	LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRKAVSLSLITVPVSHPVLTLSA	480
DB	421	LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRKAVSLSLITVPVSHPVLTLSA	480
QY	481	EALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY	540
DB	481	EALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY	540
QY	541	CTADNGFGPQRSEVSLFVTVPSRPILTLRVPRAQAVVGDLELHCEAPRSPPILYWF	600
DB	541	CTADNGFGPQRSEVSLFVTVPSRPILTLRVPRAQAVVGDLELHCEAPRSPPILYWF	600
QY	601	YHEDVTLGSSAPSGGEAFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI	660
DB	601	YHEDVTLGSSAPSGGEAFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI	660
QY	661	LTFRAPRAQAVVGDLELHCEALRGSSPILYFYHEDVTLGKISAPSGGASFNLSLITE	720
DB	661	LTFRAPRAQAVVGDLELHCEALRGSSPILYFYHEDVTLGKISAPSGGASFNLSLITE	720
QY	721	HSGIYSCDADNGLEAQRSEMWTLKVA	746
DB	721	HSGIYSCDADNGLEAQRSEMWTLKVA	746

RESULT 10
US-10-403-847-7
; Sequence 7, Application US/10403847
; Publication No. US20040030098A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLICED VARIANTS OF A HUMAN
; FILE OF INVENTION: CELL SURFACE PROTEIN WITH IMMUNOLOGICAL FOLDS, BGS5G AND BGS5H
; FILE REFERENCE: D0228 NP
; CURRENT APPLICATION NUMBER: US/10/403,847

; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: U.S. 60/368,671
; FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: U.S. 60/371,420
; FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-847-7

Query Match 76.4%; Score 746; DB 15; Length 759;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MLLWVILLVLPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTKGFRFYSPOKTKWYHR	60
DB	1	MLLWVILLVLPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTKGFRFYSPOKTKWYHR	60
QY	61	YLKKEILRETPDNILVQSGEYRCQAQSPSSPVHLDFFSSASLILOAPLSVFEQDSVV	120
DB	61	YLKKEILRETPDNILVQSGEYRCQAQSPSSPVHLDFFSSASLILOAPLSVFEQDSVV	120
QY	121	LCRAKAEVTLNNTIYKNDNVLAFLNKRDPHIFACLDKNGAYRCTGYKESCCPVSSNT	180
DB	121	LCRAKAEVTLNNTIYKNDNVLAFLNKRDPHIFACLDKNGAYRCTGYKESCCPVSSNT	180
QY	181	VKIQVEPTPRVLRASSQPIISGNPVTCTQTSLSERSDVLPRFRDDQTLGLGWS	240
DB	181	VKIQVEPTPRVLRASSQPIISGNPVTCTQTSLSERSDVLPRFRDDQTLGLGWS	240
QY	241	LSNFOITAMWSDSGFYWCKAATMPHSVISDSPRSWIQVQIPASHPVLTLSPEKALNFE	300
DB	241	LSNFOITAMWSDSGFYWCKAATMPHSVISDSPRSWIQVQIPASHPVLTLSPEKALNFE	300
QY	301	GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCRCERGASISFSLTNSGNYCTADNG	360
DB	301	GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCRCERGASISFSLTNSGNYCTADNG	360
QY	361	LGAKPSKAVSLSVTVPSHPVLNLSPPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA	420
DB	361	LGAKPSKAVSLSVTVPSHPVLNLSPPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA	420
QY	421	LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRKAVSLSLITVPVSHPVLTLSA	480
DB	421	LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRKAVSLSLITVPVSHPVLTLSA	480
QY	481	EALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY	540
DB	481	EALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY	540
QY	541	CTADNGFGPQRSEVSLFVTVPSRPILTLRVPRAQAVVGDLELHCEAPRSPPILYWF	600
DB	541	CTADNGFGPQRSEVSLFVTVPSRPILTLRVPRAQAVVGDLELHCEAPRSPPILYWF	600
QY	601	YHEDVTLGSSAPSGGEAFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI	660
DB	601	YHEDVTLGSSAPSGGEAFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI	660
QY	661	LTFRAPRAQAVVGDLELHCEALRGSSPILYFYHEDVTLGKISAPSGGASFNLSLITE	720
DB	661	LTFRAPRAQAVVGDLELHCEALRGSSPILYFYHEDVTLGKISAPSGGASFNLSLITE	720
QY	721	HSGIYSCDADNGLEAQRSEMWTLKVA	746
DB	721	HSGIYSCDADNGLEAQRSEMWTLKVA	746

RESULT 11
US-10-764-324-10460
; Sequence 10460, Application US/10764324

Publication No. US20040175739A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/764,324
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US/10/040,862
PRIOR FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10460
LENGTH: 759
TYPE: PRT
ORGANISM: Homo sapiens
US-10-764-324-10460

Query Match 76.4%; Score 746; DB 16; Length 759;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLWVLLVLPVSGQFARTPIIPLOPPWTVFQGERVLTCKGFRFYSPQTKWYHR 60
Db 1 MLWVLLVLPVSGQFARTPIIPLOPPWTVFQGERVLTCKGFRFYSPQTKWYHR 60

Qy 61 YLGKELRETDPNILEVQESGEYRCQAQGSPLSPVHLDFFSSASLILQAPLSVFEQDSV 120
Db 61 YLGKELRETDPNILEVQESGEYRCQAQGSPLSPVHLDFFSSASLILQAPLSVFEQDSV 120

Qy 121 LRCRAKAEVTLNNTYKNDNVLAFLNKRTPDHPHACLKNGAYRCTGKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTYKNDNVLAFLNKRTPDHPHACLKNGAYRCTGKESCCPVSSNT 180

Qy 181 VKIQVEPTTRVLRASSFPQISGNPVTLCETQLSLERSDVLPFRFRDDQTLGLGWS 240
Db 181 VKIQVEPTTRVLRASSFPQISGNPVTLCETQLSLERSDVLPFRFRDDQTLGLGWS 240

Qy 241 LSPNFOITAMWSKDSGFYWCXKAATMPHSVSDSPRSNTQVQIPASHPVLTLSPEKALNFE 300
Db 241 LSPNFOITAMWSKDSGFYWCXKAATMPHSVSDSPRSNTQVQIPASHPVLTLSPEKALNFE 300

Qy 301 GFKVTLHCETQDSRLTYRFRVHEGVLPRLHKSVCRCERGASISFSLTSTENSNGNYCTADNG 360
Db 301 GFKVTLHCETQDSRLTYRFRVHEGVLPRLHKSVCRCERGASISFSLTSTENSNGNYCTADNG 360

Qy 361 LGAKPSKAVSLSTVTPVSHPVNLSSPEDLIFEPAKVTLHCEAQRGSLPILYQPHHEDAA 420
Db 361 LGAKPSKAVSLSTVTPVSHPVNLSSPEDLIFEPAKVTLHCEAQRGSLPILYQPHHEDAA 420

Qy 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRKAVSLSTVTPVSHPVLTLSA 480
Db 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRKAVSLSTVTPVSHPVLTLSA 480

Qy 481 EALTTEGATVTLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
Db 481 EALTTEGATVTLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540

Qy 541 CTADNGFGPQRSEVSLFVTPVSRPILTLRVPRQAQVAVGDLLELHCEAPRGSPPILYWF 600
Db 541 CTADNGFGPQRSEVSLFVTPVSRPILTLRVPRQAQVAVGDLLELHCEAPRGSPPILYWF 600

Qy 601 YHEDVTILGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVQAHSOTISLSVTPVSRPI 660
Db 601 YHEDVTILGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVQAHSOTISLSVTPVSRPI 660

Qy 661 LTFRAPRAQAVVGDLLELHCEALRGSPILYWFYHEDVTILGKISAPSGGASFNLSLTTTE 720
Db 661 LTFRAPRAQAVVGDLLELHCEALRGSPILYWFYHEDVTILGKISAPSGGASFNLSLTTTE 720

Qy 721 HSGIYSCEADNGLEAQRSEMVTTLKVA 746
Db 721 HSGIYSCEADNGLEAQRSEMVTTLKVA 746

RESULT 12
US-10-403-847-4
Sequence 4, Application US/10403847
Publication No. US20040030098A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLIC VARIANTS OF A HUMAN
FILE REFERENCE: D0228 NP
CURRENT APPLICATION NUMBER: US/10/403,847
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: U.S. 60/368,671
PRIOR FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: U.S. 60/371,420
PRIOR FILING DATE: 2002-04-10
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 790
TYPE: PRT
ORGANISM: Homo sapiens
US-10-403-847-4

Query Match 65.9%; Score 644; DB 15; Length 790;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 103 ASLILQAPLSVFEQDSVLRCAKAEVTLNNTYKNDNVLAFLNKRTPDHPHACLKNG 162
Db 134 ASLILQAPLSVFEQDSVLRCAKAEVTLNNTYKNDNVLAFLNKRTPDHPHACLKNG 193

Qy 163 AYRCTGVKESCCPVSSNTVKIQVEPTTRVLRASSFPQISGNPVTLCETQLSLERSDV 222
Db 194 AYRCTGVKESCCPVSSNTVKIQVEPTTRVLRASSFPQISGNPVTLCETQLSLERSDV 253

Qy 223 PLRFRFRDDQTLGLGWSLSPNQITAMWSKDSGFYWCXKAATMPHSVSDSPRSNTQVQI 282
Db 254 PLRFRFRDDQTLGLGWSLSPNQITAMWSKDSGFYWCXKAATMPHSVSDSPRSNTQVQI 313

Qy 283 PASHPVLTLSPEKALNFEQTKVTLHCETQDSRLTYRFRVHEGVLPRLHKSVCRCERGASIS 342
Db 314 PASHPVLTLSPEKALNFEQTKVTLHCETQDSRLTYRFRVHEGVLPRLHKSVCRCERGASIS 373

Qy 343 FSLTSTENSNGNYCTADNGLGAKPSKAVSLSTVTPVSHPVNLSSPEDLIFEPAKVTLHCE 402
Db 374 FSLTSTENSNGNYCTADNGLGAKPSKAVSLSTVTPVSHPVNLSSPEDLIFEPAKVTLHCE 433

Qy 403 AQRGSLPILYQPHHEDAALERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRKAV 462


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/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,999
/ PRIOR FILING DATE: 2000-05-01
/ PRIOR APPLICATION NUMBER: US 60/202,084
/ PRIOR FILING DATE: 2000-05-04
/ PRIOR APPLICATION NUMBER: US 60/206,201
/ PRIOR FILING DATE: 2000-05-22
/ PRIOR APPLICATION NUMBER: US 60/218,950
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: US 60/222,903
/ PRIOR FILING DATE: 2000-08-03
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 10979
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 10461
/ LENGTH: 592
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-057-475B-10461

Query Match      57.3%; Score 560; DB 15; Length 592;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MLLWILLVAPVSGQFARTPRPIIFLOPPWTTVFQGERVLTICKGFFYSPQTKWYHR 60
Db      1 MLLWILLVAPVSGQFARTPRPIIFLOPPWTTVFQGERVLTICKGFFYSPQTKWYHR 60

Qy      61 YLGKEILRETPDNILEVQESGYRCAQGSPLSSPVHLDFFSSASLILOAPLSVFEQSVV 120
Db      61 YLGKEILRETPDNILEVQESGYRCAQGSPLSSPVHLDFFSSASLILOAPLSVFEQSVV 120

Qy      121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTRDHPHACLDKNGAYRCTGYKESCCPVSSNT 180
Db      121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTRDHPHACLDKNGAYRCTGYKESCCPVSSNT 180

Qy      181 VKIQVEPPTRPVLRASSFQPIISGNPVTLTCTQLSLERSDVPFLRFRFRDDOTLGLWS 240
Db      181 VKIQVEPPTRPVLRASSFQPIISGNPVTLTCTQLSLERSDVPFLRFRFRDDOTLGLWS 240

Qy      241 LSPNQITAMWSKDSGFYWCKAATMPHSVSDSPRSWTOVIPASHPVLTLSPEKALNFE 300
Db      241 LSPNQITAMWSKDSGFYWCKAATMPHSVSDSPRSWTOVIPASHPVLTLSPEKALNFE 300

Qy      301 GTKVTLHCETQEDSLRTLRYFHEGVPLRHKSVCRCERGASISFSLTTENSGNYICTADNG 360
Db      301 GTKVTLHCETQEDSLRTLRYFHEGVPLRHKSVCRCERGASISFSLTTENSGNYICTADNG 360

Qy      361 LGAKPSKAVSLSVTPVPSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Db      361 LGAKPSKAVSLSVTPVPSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420

Qy      421 LERRANSAGGVAISFSLTAHSGNYICTADNGFGPQRSKAVSLSVTPVPSHPVLTLSA 480
Db      421 LERRANSAGGVAISFSLTAHSGNYICTADNGFGPQRSKAVSLSVTPVPSHPVLTLSA 480

Qy      481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSPFSFSLTEGHSNYY 540
Db      481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSPFSFSLTEGHSNYY 540

Qy      541 CTADNGFGPQRSEVVSFLVFT 560
Db      541 CTADNGFGPQRSEVVSFLVFT 560
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RESULT 15
US-10-154-884B-10461
/ Sequence 10461, Application US/10154884B
/ Publication No. US20040005561A1
/ GENERAL INFORMATION:
/ APPLICANT: Gaiger, Alexander
/ APPLICANT: Algate, Paul A.
/ APPLICANT: Mannion, Jane
```

```
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Corixa Corporation
/ TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
/ TITLE OF INVENTION: Hematological Malignancies
/ FILE REFERENCE: 014058-013521US
/ CURRENT APPLICATION NUMBER: US/10/154,884B
/ CURRENT FILING DATE: 2002-05-23
/ PRIOR APPLICATION NUMBER: US 60/186,126
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: US 60/190,479
/ PRIOR FILING DATE: 2000-03-17
/ PRIOR APPLICATION NUMBER: US 60/200,545
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 60/200,303
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,779
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,999
/ PRIOR FILING DATE: 2000-05-01
/ PRIOR APPLICATION NUMBER: US 60/202,084
/ PRIOR FILING DATE: 2000-05-04
/ PRIOR APPLICATION NUMBER: US 60/206,201
/ PRIOR FILING DATE: 2000-05-22
/ PRIOR APPLICATION NUMBER: US 60/218,950
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: US 60/222,903
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 11290
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 10461
/ LENGTH: 592
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-154-884B-10461

Query Match      57.3%; Score 560; DB 15; Length 592;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MLLWILLVAPVSGQFARTPRPIIFLOPPWTTVFQGERVLTICKGFFYSPQTKWYHR 60
Db      1 MLLWILLVAPVSGQFARTPRPIIFLOPPWTTVFQGERVLTICKGFFYSPQTKWYHR 60

Qy      61 YLGKEILRETPDNILEVQESGYRCAQGSPLSSPVHLDFFSSASLILOAPLSVFEQSVV 120
Db      61 YLGKEILRETPDNILEVQESGYRCAQGSPLSSPVHLDFFSSASLILOAPLSVFEQSVV 120

Qy      121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTRDHPHACLDKNGAYRCTGYKESCCPVSSNT 180
Db      121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTRDHPHACLDKNGAYRCTGYKESCCPVSSNT 180

Qy      181 VKIQVEPPTRPVLRASSFQPIISGNPVTLTCTQLSLERSDVPFLRFRFRDDOTLGLWS 240
Db      181 VKIQVEPPTRPVLRASSFQPIISGNPVTLTCTQLSLERSDVPFLRFRFRDDOTLGLWS 240

Qy      241 LSPNQITAMWSKDSGFYWCKAATMPHSVSDSPRSWTOVIPASHPVLTLSPEKALNFE 300
Db      241 LSPNQITAMWSKDSGFYWCKAATMPHSVSDSPRSWTOVIPASHPVLTLSPEKALNFE 300

Qy      301 GTKVTLHCETQEDSLRTLRYFHEGVPLRHKSVCRCERGASISFSLTTENSGNYICTADNG 360
Db      301 GTKVTLHCETQEDSLRTLRYFHEGVPLRHKSVCRCERGASISFSLTTENSGNYICTADNG 360

Qy      361 LGAKPSKAVSLSVTPVPSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Db      361 LGAKPSKAVSLSVTPVPSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420

Qy      421 LERRANSAGGVAISFSLTAHSGNYICTADNGFGPQRSKAVSLSVTPVPSHPVLTLSA 480
Db      421 LERRANSAGGVAISFSLTAHSGNYICTADNGFGPQRSKAVSLSVTPVPSHPVLTLSA 480

Qy      481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSPFSFSLTEGHSNYY 540
Db      481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSPFSFSLTEGHSNYY 540
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Db	481	EALTFEGATVTLHCEVQSGPQILYQFYHEDVPLWSSSTPSVGRVSFSLTEGHSNYY	540
Qy	541	CTADNGFGPQSEVVSFLVT	560
Db	541	CTADNGFGPQSEVVSFLVT	560

Search completed: November 18, 2004, 13:17:17
Job time : 159 secs

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: November 18, 2004, 12:57:59 ; Search time 25 seconds
(without alignments)
2591.707 Million cell updates/sec

Title: US-09-724-254A-41

Perfect score: 977

Sequence: 1 MLLWILLVLAPVSGQPART.....KVASTPVSGSLFLASSAPHR 977

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents_AA.*

- 1: /cgm2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgm2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgm2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgm2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgm2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	0.9	51	3	US-08-569-147-91
2	9	0.9	107	3	US-08-838-682-16
3	9	0.9	107	3	US-08-895-914-16
4	9	0.9	107	3	US-09-357-710A-16
5	9	0.9	107	4	US-09-357-707-16
6	9	0.9	107	4	US-09-357-708-16
7	9	0.9	109	5	PCT-US92-02044-2
8	9	0.9	121	3	US-08-838-682-11
9	9	0.9	121	3	US-08-895-914-11
10	9	0.9	121	3	US-09-357-710A-11
11	9	0.9	121	4	US-09-357-707-11
12	9	0.9	121	4	US-09-357-708-11
13	8	0.8	36	3	US-09-227-357-550
14	8	0.8	107	2	US-08-888-366-14
15	8	0.8	107	2	US-08-888-366-20
16	8	0.8	107	2	US-08-888-366-26
17	8	0.8	138	4	US-09-252-991A-26931
18	8	0.8	230	3	US-09-485-737B-102
19	8	0.8	233	3	US-09-485-737B-89
20	8	0.8	235	3	US-09-485-737B-93
21	8	0.8	240	3	US-09-485-737B-91
22	8	0.8	261	4	US-09-245-764-7
23	8	0.8	267	3	US-09-485-737B-2
24	8	0.8	469	4	US-09-538-092-948
25	8	0.8	541	3	US-09-485-737B-85
26	8	0.8	711	3	US-09-485-737B-90
27	8	0.8	906	1	US-08-486-270-2

28	8	0.8	906	3	US-08-367-264-2	Sequence 2, Appli
29	8	0.8	906	4	US-09-153-757-2	Sequence 2, Appli
30	8	0.8	906	4	US-09-459-715-2	Sequence 2, Appli
31	8	0.8	906	5	PCT-US91-09422-17	Sequence 17, Appl
32	8	0.8	1056	2	US-08-687-289A-7	Sequence 7, Appli
33	8	0.8	1056	2	US-08-687-289A-8	Sequence 8, Appli
34	8	0.8	1056	4	US-09-435-897-7	Sequence 7, Appli
35	8	0.8	1056	4	US-09-435-897-8	Sequence 8, Appli
36	8	0.8	1194	3	US-08-538-526-1	Sequence 1, Appli
37	8	0.8	1199	1	US-08-041-538-2	Sequence 2, Appli
38	8	0.8	1199	1	US-08-463-642-2	Sequence 2, Appli
39	8	0.8	1199	1	US-08-465-602-2	Sequence 2, Appli
40	8	0.8	1199	2	US-08-465-157-2	Sequence 2, Appli
41	8	0.8	1199	5	PCT-US91-09422-2	Sequence 6, Appli
42	8	0.8	1219	2	US-08-687-289A-6	Sequence 6, Appli
43	8	0.8	1219	4	US-09-435-897-6	Sequence 7, Appli
44	7	0.7	10	3	US-08-581-662-7	Sequence 7, Appli
45	7	0.7	10	4	US-09-664-295-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-569-147-91
; Sequence 91, Application US/08569147
; Patent No. 6180377
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANISED ANTIBODIES
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESS: No. 6180377ris, LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,147
; FILING DATE: 25-March-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0047
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-569-147-91

Query Match 0.9%; Score 9; DB 3; Length 51;
Best Local Similarity 100.0%; Pred No. 0.59; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 37 GERVTLTK 45
| | | | |
Db 40 GERVTLTK 48

RESULT 2

US-08-838-682-16
; Sequence 16, Application US/08895914
; Patent No. 6107090
; GENERAL INFORMATION:
; APPLICANT: Bander M.D., Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE
; TITLE OF INVENTION: CANCER
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603-1051
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,682
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/016,976
; FILING DATE: 06-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/022,125
; FILING DATE: 18-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1172
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-682-16

Query Match 0.9%; Score 9; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GERVTLTK 45
Db 16 GERVTLTK 24

RESULT 3
US-08-895-914-16
; Sequence 16, Application US/08895914
; Patent No. 6136311
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603-1051
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/895,914
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/016,976
; FILING DATE: 06-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/022,125
; FILING DATE: 18-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/838,682
; FILING DATE: 09-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1173
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-895-914-16

Query Match 0.9%; Score 9; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GERVTLTK 45
Db 16 GERVTLTK 24

RESULT 4
US-09-357-710A-16
; Sequence 16, Application US/09357710A
; Patent No. 6290956
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: Lois M. Kwasiogoch: BZL 242/025
; CURRENT APPLICATION NUMBER: US/09/357,710A
; CURRENT FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 16
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-357-710A-16

Query Match 0.9%; Score 9; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GERVTLTK 45
Db 16 GERVTLTK 24

RESULT 5

US-09-357-707-16
; Sequence 16, Application US/09357707
; Patent No. 6649163
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/078
; CURRENT APPLICATION NUMBER: US/09/357,707
; CURRENT FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/895,914
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-357-707-16

Query Match 0.9%; Score 9; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 GERVLTCK 45
Db 16 GERVLTCK 24

RESULT 6

US-09-357-708-16
; Sequence 16, Application US/09357708
; Patent No. 6770450
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/028
; CURRENT APPLICATION NUMBER: US/09/357,708
; CURRENT FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/895,914
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-357-708-16

Query Match 0.9%; Score 9; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 GERVLTCK 45
Db 16 GERVLTCK 24

RESULT 7

PCT-US92-02044-2
; Sequence 2, Application PC/TUS9202044

; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: SATO, Vicki L.
; APPLICANT: CHISHOLM, Patricia L.
; APPLICANT: WALLNER, Barbara P.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES RECOGNIZING
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 875 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02044
; FILING DATE: 19920312
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/667,975
; FILING DATE: 12-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B150CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 715-0600
; TELEFAX: (212) 715-0673
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-02044-2

Query Match 0.9%; Score 9; DB 5; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 GERVLTCK 45
Db 16 GERVLTCK 24

RESULT 8

US-08-838-682-11
; Sequence 11, Application US/08938682
; Patent No. 6107090
; GENERAL INFORMATION:
; APPLICANT: Bander M.D., Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603-1051
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30


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; SEQ ID NO 11
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-357-707-11

Query Match      0.9%; Score 9; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      37 GERVTLTK 45
Db      22 GERVTLTK 30

RESULT 12
US-09-357-708-11
; Sequence 11, Application US/09357708
; Patent No. 6770450
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/028
; CURRENT APPLICATION NUMBER: US/09/357,708
; CURRENT FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/895,914
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-357-708-11

Query Match      0.9%; Score 9; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      37 GERVTLTK 45
Db      22 GERVTLTK 30

RESULT 13
US-09-227-357-550
; Sequence 550, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732

; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 550
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-227-357-550

Query Match      0.8%; Score 8; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      147 KRTDFHIP 154
Db      27 KRTDFHIP 34

RESULT 14
US-08-888-366-14
; Sequence 14, Application US/08888366
```

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; Patent No. 5972656
; GENERAL INFORMATION:
; APPLICANT: Lopez, Osvaldo
; APPLICANT: Wylie, Dwane E.
; APPLICANT: Wagner, Fred W.
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,366
; FILING DATE: 03-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/187,407
; FILING DATE: 27-JAN-1994
; APPLICATION NUMBER: US 07/990,542
; FILING DATE: 14-DEC-1992
; APPLICATION NUMBER: US 07/493,299
; FILING DATE: 14-MAR-1990
; APPLICATION NUMBER: US 07/324,392
; FILING DATE: 14-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.39USC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-888-366-14

Query Match 0.8%; Score 8; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 GERVTLTC 44
Db 16 GERVTLTC 23

RESULT 15
US-08-888-366-20
; Sequence 20, Application US/08888366
; Patent No. 5972656
; GENERAL INFORMATION:
; APPLICANT: Lopez, Osvaldo
; APPLICANT: Wylie, Dwane E.
; APPLICANT: Wagner, Fred W.
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
; CITY: Minneapolis
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; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,366
; FILING DATE: 03-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/187,407
; FILING DATE: 27-JAN-1994
; APPLICATION NUMBER: US 07/990,542
; FILING DATE: 14-DEC-1992
; APPLICATION NUMBER: US 07/493,299
; FILING DATE: 14-MAR-1990
; APPLICATION NUMBER: US 07/324,392
; FILING DATE: 14-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.39USC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-888-366-20

Query Match 0.8%; Score 8; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 GERVTLTC 44
Db 16 GERVTLTC 23

Search completed: November 18, 2004, 13:06:23
Job time : 26 secs
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PR 02-JUN-1999; 99WO-US012252.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021090.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 06-JAN-2000; 2000WO-US000219.
 PR 11-FEB-2000; 2000WO-US000376.
 PR 18-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004341.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 16-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021086.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 28-AUG-2001; 2001US-00941992.
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski P;
 PI Grimaldi JC, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood MT;
 PI Zhang Z;
 XX
 WPI: 2003-247083/24.
 DR N-PSDB; AEX80219.
 XX
 PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
 PT are therapeutically useful for enhancing immune response and in cancer
 PT treatments.
 XX
 PS Claim 12; Fig 83; 648pp; English.
 XX
 CC The invention describes an isolated human PRO polypeptide. The PRO
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
 CC in modulating at least one biological activity of a cell expressing a PRO
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
 CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
 CC useful for treating conditions or disorders where angiogenesis would be
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are
 CC useful for treating cancerous tumours. PRO812 inhibits vascular
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
 CC cells and is thus useful for inhibiting endothelial cell growth in
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing

CC immune response. PRO828, PRO826, PRO1068 or PRO132 enhance survival of
 CC retinal neurons cells (PRO132 is also enhances survival/proliferation of
 CC rod photoreceptor cells) and therefore are useful for treating retinal
 CC disorders of injuries, e.g. retinitis pigmentosum, AMD PRO819, PRO813
 CC and PRO1065 induce proliferation of mammalian kidney mesangial cells,
 CC and therefore are useful for treating kidney disorders associated with
 CC decreased mesangial cell function such as Berger disease or Crohn's
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
 CC proliferation and/or redifferentiation of chondrocytes in culture and are
 CC thus useful for treating sports injuries and arthritis. This is the
 CC amino acid sequence of a novel human PRO protein
 XX
 SQ Sequence 124 AA;
 Query Match 10.4%; Score 102; DB 6; Length 124;
 Best Local Similarity 100.0%; Pred. No. 7.6e-89; Indels 0; Gaps 0;
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLWVILLVLPVSGQFARTPRPIIFLPQPPWTVFQGERVTITCKGFRYSQKTKWYHR 60
 DB 1 MLLWVILLVLPVSGQFARTPRPIIFLPQPPWTVFQGERVTITCKGFRYSQKTKWYHR 60
 QY 61 YLCKEILRETTPNILEVQESGEYRCOAQGSPLSSPVHLDFFS 102
 DB 61 YLCKEILRETTPNILEVQESGEYRCOAQGSPLSSPVHLDFFS 102
 RESULT 14
 ABUS2589
 ID ABUS2589 standard; protein; 124 AA.
 AC ABUS2589;
 XX
 DT 26-JUN-2003 (first entry)
 XX
 DE Human secreted/transmembrane protein PRO820.
 XX
 KW Human; PRO; secreted protein; transmembrane protein;
 KW Cardiac insufficiency disorders; angiogenesis; wound healing;
 KW cancerous tumour; immune response; retinal disorder; sight loss;
 KW retinitis pigmentosum; age-related macular degeneration; AMD;
 KW kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;
 KW Crohn's disease; sports injury; arthritis.
 XX
 OS Homo sapiens.
 XX
 PN US2003032023-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 14-NOV-2001; 2001US-00990711.
 XX
 PR 16-JUN-1997; 97US-0049787P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 05-NOV-1997; 97WO-US020069.
 PR 12-NOV-1997; 97US-0065186P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 25-FEB-1998; 98US-0075245P.
 PR 28-MAR-1998; 98US-0078510P.
 PR 28-APR-1998; 98US-0083322P.
 PR 07-MAY-1998; 98US-0084600P.
 PR 28-MAY-1998; 98US-0087106P.
 PR 02-JUN-1998; 98US-0087609P.
 PR 02-JUN-1998; 98US-0087759P.
 PR 03-JUN-1998; 98US-0087827P.
 PR 04-JUN-1998; 98US-0088021P.
 PR 04-JUN-1998; 98US-0088025P.
 PR 04-JUN-1998; 98US-0088026P.
 PR 04-JUN-1998; 98US-0088028P.
 PR 04-JUN-1998; 98US-0088029P.

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OM protein - protein search, using sw model

Run on: November 18, 2004, 12:55:33 ; Search time 47 Seconds
(without alignments)
2000.080 Million cell updates/sec

Title: US-09-724-254A-41
Perfect score: 977
Sequence: 1 MLLWVILLVLPVSGQFART.....KVASTPVGSLFLASSAPHR 977

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	2.4	255	2 JC7593	SH2 domain-contain
2	9	0.9	111	2 D37266	Ig kappa chain V r
3	9	0.9	118	2 I33932	Ig kappa chain pre
4	9	0.9	136	1 KWS21	Ig kappa chain pre
5	8	0.8	167	2 AC314	hypothetical membr
6	8	0.8	194	2 E75150	hypothetical prote
7	8	0.8	207	2 I30609	T-cell surface gly
8	8	0.8	270	2 A34636	Fc-gamma receptor
9	8	0.8	280	2 I55577	Fc gamma (IG) rec
10	8	0.8	281	2 F72759	hypothetical prote
11	8	0.8	300	2 E84310	hypothetical prote
12	8	0.8	312	2 E83740	hypothetical prote
13	8	0.8	315	2 S17952	acyltransferase (E
14	8	0.8	322	2 T36841	probable secreted
15	8	0.8	344	2 A41357	Fc gamma (IG) rec
16	8	0.8	374	1 A39878	Fc gamma (IG) rec
17	8	0.8	452	2 F69906	conserved hypotet
18	8	0.8	469	1 DMHU	desmin - human
19	8	0.8	469	2 A24783	desmin - golden ha
20	8	0.8	469	2 A54104	desmin - mouse
21	8	0.8	469	2 I52469	desmin - rat
22	8	0.8	477	2 T50580	hypothetical prote
23	8	0.8	536	2 T04222	hypothetical prote
24	8	0.8	647	1 I48737	LIM protein kinase
25	8	0.8	1199	2 A41939	G protein-coupled
26	8	0.8	1356	2 T18521	beta transducin-li
27	8	0.8	1932	2 S53409	probable membrane
28	7	0.7	67	2 F97798	hypothetical prote
29	7	0.7	69	2 A71330	hypothetical prote

30	7	0.7	80	2 E71430	hypothetical prote
31	7	0.7	89	2 H90927	hypothetical prote
32	7	0.7	89	2 D85776	hypothetical prote
33	7	0.7	89	2 E64926	hypothetical prote
34	7	0.7	98	2 T46381	hypothetical prote
35	7	0.7	104	2 S09780	hypothetical prote
36	7	0.7	112	2 A42242	T-cell receptor al
37	7	0.7	115	2 T12517	hypothetical prote
38	7	0.7	123	2 E95960	hypothetical membr
39	7	0.7	126	2 C75346	competence protein
40	7	0.7	129	2 T22189	hypothetical prote
41	7	0.7	129	2 H70727	hypothetical prote
42	7	0.7	131	2 S75262	sensory transducti
43	7	0.7	132	2 I71935	MHC class II I-A-a
44	7	0.7	133	2 AB2869	conserved hypotet
45	7	0.7	135	2 B72768	hypothetical prote

ALIGNMENTS

RESULT 1

JC7593
SH2 domain-containing phosphatase anchor protein la - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7593
R;Xu, M.; Zhao, R.; Zhao, Z.J.
Biochem. Biophys. Res. Commun. 280, 768-775, 2001
A;Title: Molecular cloning and characterization of SPAP1, an inhibitory receptor.
F;27-135/Domain: extracellular #status predicted <EXT>
F;68-115/Domain: immunoglobulin-like #status predicted <IGL>
F;148-169/Domain: transmembrane region #status predicted <TM>
F;195-255/Domain: intracellular #status predicted <INT>
A;Accession: JC7593
A;Molecule type: mRNA
A;Residues: 1-255 <XUA>
A;Cross-references: UNIPROT:Q9BZ16; GB:AF319438
C;Genetics:
A;Gene: Spapla
A;Map position: 1q21
C;Introns: 135/1; 174/1; 183/2; 212/1; 234/1; 243/3
C;Keywords: glycoprotein
F;27-135/Domain: extracellular #status predicted <EXT>
F;68-115/Domain: immunoglobulin-like #status predicted <IGL>
F;148-169/Domain: transmembrane region #status predicted <TM>
F;195-255/Domain: intracellular #status predicted <INT>

Query Match 2.4%; Score 23; DB 2; Length 255;
Best Local Similarity 100.0%; Pred. No. 5.2e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 618 ASFNLSITAEHSNGYSCAANGL 640
Db 99 ASFNLSITAEHSNGYSCAANGL 121

RESULT 2

D37266
Ig kappa chain V region (129) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
C;Accession: D37266
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti-
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: D37266
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-111 <RUF>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;19-93/Domain: immunoglobulin homology <IMV>

Query Match 0.9%; Score 9; DB 2; Length 111;

Best Local Similarity 100.0%; Pred. No. 1.1; Mismatches 0; Conservative 0; Indels 0; Gaps 0;

QY 37 GERVTLTCK 45
|||||
Db 19 GERVTLTCK 27

RESULT 3
133932
Ig kappa chain precursor V region (E7) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C:Accession: I33932
R:Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 4824-4828, 1989
A:Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-line genes
A:Reference number: A33932; MUID:89282823; PMID:2499887
A:Accession: I33932
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-118 <BAC>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:39-113/Domain: immunoglobulin homology <IMM>

Query Match 0.9%; Score 9; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.2; Mismatches 0; Indels 0; Gaps 0;

QY 37 GERVTLTCK 45
|||||
Db 39 GERVTLTCK 47

RESULT 4
KVMS21
Ig kappa chain precursor V region (MOPC 21) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1980 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C:Accession: A93736; A90262; B49982; A01917
R:Hamlyn, P.H.; Gait, M.J.; Milstein, C.
Nucleic Acids Res. 9, 4485-4494, 1981
A:Title: Complete sequence of an immunoglobulin mRNA using specific priming and the dideoxy method
A:Reference number: A93736; MUID:82059477; PMID:6170937
A:Accession: A93736
A:Molecule type: mRNA
A:Residues: 1-136 <HAM>
A:Cross-references: UNIPROT:P01634
R:Swasti, J.; Milstein, C.
Biochem. J. 128, 427-444, 1972
A:Title: The complete amino acid sequence of a mouse kappa light chain.
A:Reference number: A90262; MUID:73053310; PMID:4638343
A:Contents: myeloma protein MOPC 21
A:Accession: A90262
A:Molecule type: protein
A:Residues: 30-136 <SVB>
R:Linn, C.; Kleber-Emmons, T.; Villalobos, A.P.; Foster, M.H.; Wahlgren, C.; Kleyman, T.R.
J. Biol. Chem. 269, 2805-2813, 1994
A:Title: Topology of an amiloride-binding protein.
A:Reference number: A49982; MUID:94132051; PMID:8300613
A:Accession: B49982
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 30-136 <LIN>
A:Cross-references: GB:I24803; NID:9452098; PIDN:AAC37684.1; PID:g452099
A:Experimental source: clone BA7.1
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-136/Product: Ig kappa chain V region (MOPC 21) #status experimental <MAT>

F:45-119/Domain: immunoglobulin homology <IMM>
F:125-136/Region: J segment (JK2)
F:52-117/Disulfide bonds: #status predicted

Query Match 0.9%; Score 9; DB 1; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.4; Mismatches 9; Conservative 0; Indels 0; Gaps 0;

QY 37 GERVTLTCK 45
|||||
Db 45 GERVTLTCK 53

RESULT 5
AC3314
Hypothetical membrane spanning protein BMEI0497 [imported] - Brucella melitensis (strain C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AC3314
R:DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujar, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, M.; Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AC3314
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-167 <KUR>
A:Cross-references: UNIPROT:Q9VIE7; GB:AE008917; PIDN:AAI51678.1; PID:gl7982410; GSPDB:GB:AE008917
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI0497
A:Map position: 1

Query Match 0.8%; Score 8; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 15; Mismatches 8; Conservative 0; Indels 0; Gaps 0;

QY 861 GLAAGALL 868
|||||
Db 81 GLAAGALL 88

RESULT 6
E75150
Hypothetical protein PAB0241 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: E75150
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A:Reference number: A75001
A:Accession: E75150
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-194 <RAW>
A:Cross-references: UNIPROT:Q9V1R5; GB:AJ248284; GB:AL096836; NID:g5457730; PIDN:CAB49284
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB0241

Query Match 0.8%; Score 8; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 17; Mismatches 8; Conservative 0; Indels 0; Gaps 0;

QY 4 WVILLVLA 11
|||||
Db 27 WVILLVLA 34

RESULT 7
150609

T-cell surface glycoprotein CD8 beta chain - chicken
C:Species: Gallus gallus (chicken)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50609; 837237
R:Tragakes, C.A.; Kong, F.K.; Paramithiotis, E.; Chen, C.L.; Ratcliffe, M.J.; Davison, J.; Immunol. 154, 4485-4494, 1995
A:Title: Identification and analysis of the expression of CD8 alpha beta and CD8 alpha A lymphocytes.
A:Reference number: I50609; MUID:95238946; PMID:7722305
A:Accession: I50609
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-207 <TR>
A:Cross-references: UNIPROT:Q90769; EMBL:Z26484; NID:G403300; PIDN:CAA81258.1; PID:G4033
C:Superfamily: T-cell surface glycoprotein CD8 beta chain; immunoglobulin homology
C:Keywords: glycoprotein

Query Match 0.8%; Score 8; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 862 LAAGALLL 869
|||
Db 175 LAAGALLL 182

RESULT 8
A34636
Fc-gamma receptor II precursor - guinea pig
C:Species: Cavia porcellus (guinea pig)
C>Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 16-Jul-1999
C:Accession: A34636
R:Tomimaga, M.; Sakata, A.; Ohmura, T.; Yamashita, T.; Koyama, J.; Onoue, K. Biochem. Biophys. Res. Commun. 168, 683-689, 1990
A:Title: The structure and expression of the guinea pig Fc receptor for IgG1 and IgG2 (F3/37-88/Domain: immunoglobulin homology <IMM>
A:Reference number: A34636; MUID:90241239; PMID:1692213
A:Accession: A34636
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-270 <TOM>
A:Cross-references: GB:M35272
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: immunoglobulin receptor
F:37-88/Domain: immunoglobulin homology <IMM>

Query Match 0.8%; Score 8; DB 2; Length 270;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 SGEYRCQA 87
|||
Db 81 SGEYRCQA 88

RESULT 9
I55577
Fc gamma (IgG) receptor I-B splice form 1 precursor - human
N:Alternate names: CD64
N:Contains: Fc-gamma (IgG) receptor I-B splice form 2
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I55577; I70303
R:Portges, A.J.; Redecha, P.B.; Doebele, R.; Pan, L.C.; Salmon, J.E.; Kimberley, R.P. J. Clin. Invest. 90, 2102-2109, 1992
A:Title: Novel Fc gamma receptor I family gene products in human mononuclear cells.
A:Reference number: I55577; MUID:93055454; PMID:1430234
A:Accession: I55577
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-280 <RES>
A:Cross-references: UNIPROT:Q92637; GB:L03419; NID:g182460; PIDN:AAA35825.1; PID:g292023
A>Note: splice form B1
A:Accession: I70303

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-103-153.'A'.155-280 <RE2>
A:Cross-references: GB:L03420; NID:g182461; PIDN:AAA35826.1; PID:g292024
A:Experimental source: mononuclear cells
A>Note: Splice form B2
C:Comment: This receptor does not bind monomeric IgG with high affinity.
C:Genetics:
A:Gene: GDB:FCGR1B; CD64
A:Cross-references: GDB:135923; OMIM:601502
A:Map Position: 1p12-1p12
C:Superfamily: Fc gamma receptor I; immunoglobulin homology
C:Keywords: alternative splicing; glycoprotein; immunoglobulin receptor; transmembrane p
F:117-170/Domain: immunoglobulin homology <IMM>

Query Match 0.8%; Score 8; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 489 TVTLHCEV 496
|||
Db 38 TVTLHCEV 45

RESULT 10
F72759
hypothetical protein APE0067 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: F72759
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kawa
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: F72759
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-281 <KAW>
A:Cross-references: UNIPROT:Q9Y34; DBJ:AF000058; NID:g5103388; PIDN:BAA78976.1; PID:g51
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE0067
C:Superfamily: probable ribose ABC transporter rbsC-2

Query Match 0.8%; Score 8; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 860 AGLAAGAL 867
|||
Db 59 AGLAAGAL 66

RESULT 11
E84310
hypothetical protein Vng1572c [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: E84310
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: E84310
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-300 <STO>
A:Cross-references: UNIPROT:Q9HPL8; GB:AE004437; NID:g10581055; PIDN:AAG19849.1; GSPDB:G
C:Genetics:

```

A:Gene: VNG1572C
C:Superfamily: uncharacterized conserved protein MJ1598

Query Match      0.8%; Score 8; DB 2; Length 300;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      860 AGLAAGAL 867
DB      178 AGLAAGAL 185
      |||||
      |||||

RESULT 12
E83740
hypothetical protein BH0725 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: E83740
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: E83740
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-312 <STO>
A:Cross-references: UNIPROT:Q9KEX4; GB:AP001509; GB:BA000004; NID:G10173176; PIDN:BA8044
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0725
C:Superfamily: hypothetical protein yded

Query Match      0.8%; Score 8; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      862 LAAGALLL 869
DB      44 LAAGALLL 51
      |||||
      |||||

RESULT 13
S17952
acyltransferase (EC 2.3.1.-) luxD - Photobacterium leiognathi
C:Species: Photobacterium leiognathi
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: S17952
R:Lee, C.Y.; Szittner, R.B.; Meighen, E.A.
Eur. J. Biochem. 201, 161-167, 1991
A:Title: The lux genes of the luminous bacterial symbiont, Photobacterium leiognathi, of
coli.
A:Reference number: S17836; MUID:92007870; PMID:1915359
A:Accession: S17952
A:Molecule type: DNA
A:Residues: 1-315 <LEE>
A:Cross-references: UNIPROT:P21309; EMBL:M63594; NID:G150687; PIDN:AAA25617.1; PID:G1506
C:Genetics:
A:Gene: luxD
C:Superfamily: acyltransferase (EC 2.3.1.-) luxD
C:Keywords: acyltransferase

Query Match      0.8%; Score 8; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      387 PEDLIEFG 394
DB      164 PEDLIEFG 171
      |||||
      |||||

RESULT 14
T36841
probable secreted protein - Streptomyces coelicolor

```

```

C:Species: Streptomyces coelicolor
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T36841
R:Oliver, K.; Harris, D.; Parkhill, J.; Barrrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z21615
A:Accession: T36841
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-322 <OLI>
A:Cross-references: UNIPROT:O88063; EMBL:AL031541; PIDN:CAA20817.1; GSPDB:GN00070; SCOREDI
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SCI35.28

```

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Query Match      0.8%; Score 8; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY      611 SAPSGGEA 618
DB      56 SAPSGGEA 63
      |||||
      |||||

```

```

RESULT 15
A41357
Fc gamma (IgG) receptor I (high affinity) form b - human
N:Alternate names: CD64
C:Species: Homo sapiens (man)
C>Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004
C:Accession: A41357; S03019
R:Allen, J.M.; Seed, B.
Science 243, 378-381, 1989
A:Title: Isolation and expression of functional high-affinity Fc receptor complementary I
A:Reference number: A41357; MUID:89100284; PMID:2911749
A:Accession: A41357
A:Molecule type: mRNA
A:Residues: 1-344 <ALLI>
A:Cross-references: UNIPROT:P12314; GB:X14355; GB:M21090; NID:G31333; PIDN:CAA32536.1; PJ
R:Allen, J.M.; Seed, B.
Nucleic Acids Res. 16, 11824, 1988
A:Title: Nucleotide sequence of three cDNAs for the human high affinity Fc receptor (FCR)
A:Reference number: S03018; MUID:89098339; PMID:2974947
A:Accession: S03019
A:Molecule type: mRNA
A:Residues: 1-344 <ALL2>
A:Cross-references: EMBL:X14355; NID:G31333; PIDN:CAA32536.1; PID:G31334
A:Note: the authors translated the codon ACT for residue 25 as Ala
C:Superfamily: Fc gamma receptor I; immunoglobulin homology
C:Keywords: alternative splicing; immunoglobulin receptor; transmembrane protein
F:117-170/Domain: immunoglobulin homology <IMM>

```

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Query Match      0.8%; Score 8; DB 2; Length 344;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      489 TVTLHCEV 496
DB      38 TVTLHCEV 45
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      |||||

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Search completed: November 18, 2004, 13:05:53
Job time : 49 secs

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